

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 103887

TO: Vanessa L Ford

Location:

Art Unit: 1645

Tuesday, September 16, 2003

Case Serial Number: 09596101

From: Edward Hart

Location: Biotech-Chem Library

CM1-6B02

Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Ford,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



103887

From:

Chan, Christina

Sent:

Monday, September 15, 2003 8:51 AM Ford, Vanessa; STIC-Biotech/ChemLib RE: In re:09596101 Sequence search

Subject:

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

----Original Message-----

From:

Ford, Vanessa

Sent:

Saturday, September 13, 2003 5:15 PM

To:

Chan, Christina

Subject:

In re:09596101 Sequence search

Please search SEQ ID NO:1 and 3.

Please include interference searches. Please rush.

Vanessa L. Ford Biotechnology Patent Examiner

Office: CM1 8A16 Mailbox: CM1 8E12 Phone: 703.308.4735 Art Unit:1645

> Edward Hart Technical Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

Searcher	
Phone:	
Location:	
Date Picked Up: 41	14105
Date Completed:	
Searcher Prep/Review	:
Clerical:	
Online time:	

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALÓG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .



STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Voluntary	Results Feed	back Form
		- hit time to restrict miles.

>	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	☐ Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
·	☐ Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
A	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Co	mments:



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Result
No.
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Maximum DB
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Perfect score:
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AAY24914
AAR97362
AAB52463
AAW29455
AAW29457
AAW29456
AAB99272
ABG04199
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520.781 Million cell updates/sec
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                 Mycobacterium tube Oerskovia xanthine Oerskovia xanthine Oerskovia xanthine Bacillus circulans
                                                                                                                                                                                                       Description
                                                                                                                      Eisenia foetida co
Eisenia foetida co
Oerskovia beta-1,3
Novel human diagno
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ALIGNMENTS

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RESULT 1
AAY24915
W09931229-A2
                                                                                                                                                                                             Eisenia foetida; coelomic cytolytic factor 1; CCF-1; cancer; trypanosomal infection; bacterial infection; tumour therapy; inflammation; immunology.
        Eisenia foetida polypeptides derived from coelomic cytolytic factor 1
                              WPI; 1999-385905/32.
                                                  De Baetselier P;
                                                                                                                                                                           Eisenia foetida.
                                                                                                                                                                                                                                       Eisenia foetida coelomic cytolytic factor 1 peptide
                                                                                                                                                                                                                                                                                 AAY24915;
                                                                                                                                                                                                                                                                                                   AAY24915 standard; peptide; 13
                                                                      (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
                                                                                           17-DEC-1997;
                                                                                                               16-DEC-1998;
                                                                                                                                   24-JUN-1999
                                                                                                                                                                                                                                                           25-AUG-1999 (first entry)
                                                                                           97EP-0203974.
                                                                                                               98WO-EP08169
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RESULT 2
AAY24914
Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY24914;
                                 Claim 2; Page 48-49; 49pp; English.
                                                                                                                                                        (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
                                                                                                                                                                                                                                                                WO9931229-A2
                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eisenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY24914 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence
                                                              Eiseņia
                                                                                        N-PSDB;
                                                                                                                               De Baetselier
                                                                                                                                                                                                            16-DEC-1998;
                                                                                                                                                                                                                                       24-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                   inflammation;
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                                                                                       1999-385905/32.
DB; AAX83611.
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                                                           foetida polypeptides derived
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                                                                                                                                                                                                                                                                                                                                                                                                              infection; bacterial infection;
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                                                                                                                                                                                                                                                                                                                                                                                                   immunology.
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                                                                                                                                                                                  97EP-0203974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents a Eisenia foetida coelomic cytolytic tide. The CCF-1 protein has antiparasitic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNF-alpha.
                                                            from coelomic cytolytic
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The present sequence represents the Elsenia foetida coelomic cytolytic factor 1 (CCF-1). The protein has antiparasitic, antibacterial and

A novel beta-1,3-glucanase (AAR97362) from Oerskovia xanthineolytica

Claim 1; Page 42-43; 60pp;

English.

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RESULT 3
AAR97362
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                                                DNA construct encoding enzyme with beta-1,3-glucanase activity useful for modifying or degrading beta-glucan contg. material \langle the prepn. of e.g. food colourants, flavourings and yeast extra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-1,3-glucanase; Cellulomonas cellulans; Bacillus subtilis; lytic enzyme; beta-glucan degradation; cell wall lysis; pigment; colorant; flavour; yeast extract; protoplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in a dose-dependent manner. The trypanolytic activity of rCCF-1 can inhibited by anti-CCF-1 and anti-tumour necrosis factor (TNF)/TIP monoclonal antibodies. Furthermore, N.N'-diacetlychitobiose inhibits
                                                                                                         WPI; 1996-222000/22.
N-PSDB; AAT29043.
                                                                                                                                                                                                                                                                                                                                                                                                                  Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory activity. Recombinant coelomic cytolytic factor 1 (rCCF-1) is trypanolytic for the African trypanosome Trypanosoma bu
                                                                                                                                                   Savva
                                                                                                                                                              Asenjo JA,
                                                                                                                                                                                         (NOVO ) NOVO-NORDISK
                                                                                                                                                                                                                    14-OCT-1994;
                                                                                                                                                                                                                                                16-ocr-1995;
                                                                                                                                                                                                                                                                           25-APR-1996
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                                                                                                                                                                                                                                                                                                                                              Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oerskovia beta-1,3-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vertebrate tumour necrosis factor-alpha (TNF-alpha), and may be used
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13; Conserv
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                                                                                                                                                                Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
. 0.00092;
ches 0;
                                                                                                                                                                Hedegaard L;
                                                    contg. material and in gs and yeast extracts
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                                                                                               RESULT 4
AAB52463
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Best Local S
Matches 9
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Best Local
                                                                                                              The present invention relates to Mycobacterium tuberculosis secreted proteins (MTSP), where the polypeptide has M. tuberculosis specific antigenic and immunogenic properties. Compositions of the invention be useful for diagnosing Mycobacterium tuberculosis infection and as vaccine against M. tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLG109 is useful for degrading or modifying beta-glucan-contg. material. Its amino acid sequence was deduced from a genomic DNA sequence (AAT29043) isolated from an O. xanthineolytica library. Recombinant beta-1,3-glucanase can be produced on a large scale using transformed host cells, esp. Bacillus subtilis DN1885 or Toc46. Protease-free beta-1,3-glucanase can be obtd. that is useful for lysing fungal cell walls, allowing recovery of intracellular proteins. The enzyme is also useful for the prepn. of protoplasts and for the prodn. of pigments, colorants, flavours, yeast extract
                                                                                                                                                                                        Claim 11; Fig 1; 60pp; English.
                                                                                                                                                                                                                     Novel Mycobacterium tuberculosis secreted polypeptides and polynucleotides useful in diagnosis, treatment and prophylaxis tuberculosis.
                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                      04-MAY-1999;
04-MAY-1999;
                                                                                              Sequence
                                                                                                                                                                                                                                                                                        Gennaro
                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB52463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB52463 standard; protein;
                                                                                                                                                                                                                   tuberculosis
                                                                                                                                                                                                                                                                                                            (PUBL-) PUBLIC HEALTH RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceuticals.
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                                                similarity
9; Conser
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9; Conser
SGEIDLIEWYGN 180
                        SGEIDIIETIGN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGEIDIMENVGN 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGEIDIIETIGN 12
                                                                                             294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                        Gomez MJ;
                                                                                                                                                                                                                                                                                                                                                                        2000WO-US12197
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99US-0132503.
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                                                          70.3%;
75.0%;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294
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                                              1;
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                                                         Score 45; I
Pred. No. 2.
                                                                                                                                                                                                                                                                                                              NEW
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; MTSP; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein #28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.33;
                                                      2.9;
                                                                    22;
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                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                tuberculosis secreted
                                                                   Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 306;
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                           0;
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SCEIDIIETIG

11

116 SCEIDIMENVG

126

Matches

8 Similarity

Conservative

3.9 3.9

18;

Length 263; Indels

0,

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0;

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RESULT 5
AAW29455
                                                                                                                               This polypeptide comprises a novel Oerskovia xanthineolytica (OX)
cenzyme that exhibits beta-1.3-glucanase (BG) activity. Its amino
cacid sequence was deduced from an isolated genomic DNA sequence
(see AAR89155). Claimed DNA constructs that encode the novel BG (see
CARW29456 for corrected sequence), a mannose binding domain (see
CARW29458) or a full-length enzyme, i.e. BG with mannose binding
CARW29458) or a full-length enzyme, i.e. BG with mannose binding
CARW29458) or a full-length enzyme, i.e. BG with mannose binding
CARW29458, can be used to produce recombinant BG
CARW29458, with or without a mannose binding domain, in fungal
CARW29458, can be used to produce used for the
CARW29458, can be used for the
CARW29458, can be ta-glucan containing material,
CARW29458, can be ta-glucan containing material,
CARW29458, can also be used for the
CARW2945
                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated beta-1,3-glucanase enzyme xanthineolytica, used particularly for for obtaining desirable products
                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 35-36; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW29455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW29455 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta-1,3-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oerskovia xanthineolytica mature beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1997-526451/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT89155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xanthineolytica
                                                                               263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ucanase; lytic enzyme; yeast;
wall; intracellular product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96DK-0000885
96DK-0000427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-DK00160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= k
164..952
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23..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                    68.8%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Halkier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLG109
Score 44; DB Pred. No. 3.9; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ŧ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hedegaard L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DSM 10297).

    obtained from Oerskovia
the lysis of microbial cells

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta glucan degradation;
purification; protoplast
                                                                                                                                                                                                                                                                                                                                                           (see
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RESULT 6
AAW29457
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                                                                                                                                                     cerskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase (BG) activity. Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89157). Claimed DNA constructs that encode the novel BG (see also AAW29455), a mannose binding domain (see AAW29458) or a full-length enzyme, i.e. BG with mannose binding domain (see AAW29458), can be used to produce recombinant BG polypeptides, with or without a mannose binding domain, in fungal cor bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, cespecially for the gentie lysis of microbial cell walls, thereby cenabiling recovery of desirable intracellular products with a reduced amount of contaminants. They can be used for the production of e.g. pigments, colourants, flavourants, yeast extracts, pharmaceuticals, food or feed compositions, and to
                                                               Query Match
Best Local
                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                          New isolated beta-1,3-glucanase enzyme - or canthineolytica, used particularly for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9739114-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-1,3-glucanase; lytic enzyme; yeast;
fungal cell wall; intracellular product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oerskovia xanthineolytica beta-1,3-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW29457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW29457 standard;
                                                                                                      Sequence
                                                                                                                                         prepare protoplasts
                                                                                                                                                                                                                                                                                                                                            This sequence comprises the polypeptide precursor of a novel
                                                                                                                                                                                                                                                                                                                                                                       Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NOVO ) NOVO-NORDISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                              for obtaining desirable products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1997-526451/48
 169
                                                  Similarity
8; Conserv
SGEIDIMENVG
                        SGEIDIIETIG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xanthineolytica LLG109 (DSM 10297).
                                                                                                                                                                                                                                                                                                                                                                     Page 42-43;
                                                                                                      303
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96DK-0000885
96DK-0000427
                                                                                                      ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-DK00160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry
                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halkier
                                                                                                                                                                                                                                                                                                                                                                       64pp; English.
                                                                                                                                             use in fusion, transformation and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303
                                                 Score 44; DB 1
Pred. No. 4.6;
2; Mismatches
                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hedegaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta glucan degradation;
purification; protoplast
                                                                                                                                                                                                                                                                                                                                                                                                            obtained from Oerskovia
he lysis of microbial cells
                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŗ,
                                                  1;
                                                                         Length 303;
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                                                  Gaps
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RESULT 7
AAW29456
Query Match
Best Local S
Matches
                                                                                                                                                                                                                    Oerskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase (BG) activity and which includes a mannose binding domain (MBD). Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89156). Claimed DNA constructs that encode the novel BG lacking a MBD (see AAW29455 and AAW29457), a MDB (see AAW29458), or the full-length enzyme can be used to produce recombinant BG polypeptides, with or without a mannose binding domain, in fungal or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oerskovia xanthineolytica beta-1,3-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW29456 standard; Protein; 435
                                                                                                                                                                            production of e.g. pigments, colour extracts, pharmaceuticals, food or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated beta-1,3-glucanase enzyme - ok
xanthineolytica, used particularly for the
for obtaining desirable products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW29456;
                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diers I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oerskovia xanthineolytica LLG109 (DSM 10297).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation;
fungal cell wall; intracellular product; purification; protoplast
                                                                                                                                                            prepare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 39-40; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence comprises the polypeptide precursor of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1997-526451/48.
8; Conserv
                                                                                                                                                         protoplasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferrer P,
                                                                                            435
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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96DK-0000427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-DK00160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=
53..435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Mannose-binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label = Mat_protein
                                                                                                                                                              for
                          68.8%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halkier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sig_peptide
                                                                                                                                                              use
                                                                                                                                                              'n
                       Score 44;
Pred. No.
                                                                                                                                                                                 colourants, flavourants, yeast ood or feed compositions, and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ή
                                                                                                                                                            fusion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hedegaard
                                                                                                                                                              transformation and cloning
                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obtained from Oerskovia
ne lysis of microbial cells
                                               18;
                                               Length 435;
       Indels
                                                                                                                                                                                      6
    0;
    Gaps
       0;
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169

SGEIDIIETIG

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RESULT 9
ABG04199
ID ABG0
XX
AC ABG(
DT 13-;
DE Nov
XX
KW Hun
KW Hor
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VX
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BOS 'Hor
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PN WO
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PPN 3/
XX
PFR 3/
XX
PR 2
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                                                                                                                                                                                                                                                                                                                                     RESULT 8
AAB99272
                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 8
          31-MAR-2000;
23-AUG-2000;
                                                                                                                 Human; chromosome mapping;
food supplement; medical in
                                       30-MAR-2001;
                                                           11-OCT-2001
                                                                             WO200175067-A2
                                                                                                Homo sapiens.
                                                                                                                                              Novel human diagnostic protein #4190
                                                                                                                                                                   13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                    The present sequence is beta-1,3-glucanase from Bacillus circulans. The protein can be used in various industrial fields such as stockbreeding, cake and bread manufacture and brewing.
                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-1,3-glucanase and beta-1,3-glucan-binding peptide and their genes
                                                                                                                                                                                                         ABG04199 standard;
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-364762/38.
N-PSDB; AAH46359, AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP2001120280-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta-1,3-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB99272 standard; protein; 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MEIJ ) MEIJI SEIKA KAISHA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus circulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus circulans beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ААВ99272;
                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                          118
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                                                                                                                                                                                                                                                                           SCEIDIIETIGN 12
                                                                                                                                                                                                                                                                                                                                                                                           Page 8-9; 12pp; Japanese.
                                                                                                                                                                                                                                                         SGEIDIMERVNN 129
                                                                                                                                                                                                                                                                                                                                     384 AA;
                                                                                                                                                                                                                                                                                                Conservative
         2000US-0540217
2000US-0649167
                                      2001WO-US08631
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-0311073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0311073
                                                                                                               mapping; gene mapping; gene therapy;
medical imaging; diagnostic; genetic (
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH46360
                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme;
                                                                                                                                                                                                                                                                                                        67.2%;
66.7%;
                                                                                                                                                                                                        185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stockbreeding; bread manufacture; brewing
                                                                                                                                                                                                                                                                                              Ņ
                                                                                                                                                                                                                                                                                                         Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                22;
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                                                                                                                                                                                                                                                                                                               Length 384
                                                                                                                                                                                                                                                                                            Indels
                                                                                                               disorder
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RESULT 10
AAU45016
ID AAU45
          AC XXX AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful in gene rating artivity of (II) or to treat disease states involving CC (II). (II) is useful in generating antibodies against it, detecting or Quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention. CC diagnostic amino acid sequence of the product dependent on the printed continue of the product of the printed continue of the printed specification, but was obtained in electronic format directly from WIPO at figure and product of the printed specific continue of the printed continue of the printed specific continue of the printed specific continue of the printed specific continue of the printed continue of the pr
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Best Local S
Matches 7
   21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                          20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                   01-NOV-2001
                                                                                                                                                                                                                                                                                     WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                            dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAPHO syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes immunogenic protein #5912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU45016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU45016 standard; Protein; 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory lesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 34558; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 GEVDDIDHLGNR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS68386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endophthalmitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEIDIIETIGNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 AA;
2000US-199047P.
2000US-208841P.
2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         synovitis; acne; pustulosis; hypertosis; thalmitis; bone; joint; central nervous sysion; acne vulgaris; enzyme linked immuno;
                                                                                                                                                                                                                                                                                                                                                                                                                        osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.5%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB
Pred. No. 15;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotide (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nervous system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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RESULT 11
ABG04191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by conzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-616774/71.
N-PSDB; AAS59524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky YAW,
                                            31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences AAU39105-AAU68017 represent Propionibacterium acnes polypeptides. The proteins and their associated DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID No 6211; 1069pp; English
                                                                                             30-MAR-2001; 2001WO-US08631
                                                                                                                                11-OCT-2001
                                                                                                                                                               WO200175067-A2
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                             Novel human diagnostic protein #4182.
                                                                                                                                                                                                                                                                                                                  13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                 ABG04191;
                                                                                                                                                                                                                                                                                                                                                                                ABG04191 standard; Protein;
             (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 GLIDIVESVGTR 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEIDIIETIGNR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Persing
                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9105-AAU68017 represent Propionibacterium acnes immunogenic The proteins and their associated DNA sequences are used in prevention and diagnosis of medical conditions caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%;
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, Jen S, Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB
Pred. No. 17;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ų.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang SS,
rter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 12
ABG04189
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polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in reacting of disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of another types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human contact of the invention.

Note: The sequence data for this patent did not appear in the printed appecification, but was obtained in electronic format directly from WIPO as for the invention.
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                                                                                                                                        31-MAR-2000;
23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome food supplement; m
                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                      11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
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2000US-0649167.
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medical imaging; diagnostic; genetic disorder.
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58.3%;
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CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
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Matches
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                                                                                 27-OCT-2000; 2000GB-0026333
24-NOV-2000; 2000GB-0028727
07-MAR-2001; 2001GB-0005640
                                                                                                                                                                                                                                                   Streptococcus agalactiae
                                                                                                                                                                                                                                                                                 Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antilnflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                   Streptococcus polypeptide SEQ
   Telford J,
                                (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC
                                                                                                                                                   29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                     02-MAY-2002.
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DB; AAS68376.
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   Masignani V,
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58.3%;
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Pred. No. 48;
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RESULT 14
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CC (Streptococcus/GBS), comprising one of 5483 sequences ($1), given in CC the specification. The proteins have antibacterial and antiinflammatory CC activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and CC antibodies that bind (I) are used in the manufacture of medicaments for CC treptococcus bacteria, particularly S. agalactiae and S. pyrogenes. CC Nucleic acids encoding (I) are used to detect Streptococcus in a CC biological sample. (I) is used to detect Streptococcus in a CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by CC Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity CC Streptococcus proteins and distinguishing/identifying CC Streptococcus proteins and selections and distinguishing/identifying CC Streptococcus proteins and selection an
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24-NOV-2000;
07-MAR-2001;
                                                                                                        (CHIR-)
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WPI; 2002-352536/38
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                                                             Telford
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8; Conserv
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                                                          Masignani V,
                                                                                                                                                                     ; 2000GB-0026333.
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; 2001GB-0005640.
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66.7%;
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Pred. No.
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RESULT 15
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Best Local S
Matches 8
         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                    WPI; 2001-639362/73.
N-PSDB; AAS68381.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                    (HYSE-) HYSEQ INC.
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2000US-0649167.
                                                                                                                                    Liu C,
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Pred. No.
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                                                                                                                                                 CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polyperase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disgraers involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess blodiversity amino acid sequences of the invention.

CC and to produce other types of data and products dependent on DNA and CC amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed cast partners are not only introducted in electronic format directly from WIPO at frame with the printed cast for this patent did not appear in the printed cast prints.
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Search completed: September 16, 2003, 11:25:53 Job time: 4.96222 secs

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US-09-159-106-2
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TITLE OF INVENTION: Activity
FILE REFERENCE: 4693 204-US
CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER FILING DATE: 1996-08-596
EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1997-04-14
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TITLE OF INVENTION: An Enzyme With -1,3-Glu
TITLE OF INVENTION: Activity
FILE REFERENCE: 4693 204-US
CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
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Sequence 13, App--
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LENGTH: 303
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SOFTWARE: FastSEQ for
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APPLICANT: Hedegaard, Lisbeth
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APPLICANT: Diers, Ivan
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APPLICANT: Diers, Ivan
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LENGTH: 43
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APPLICANT: Hedegaard, Lisb
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nandabalan, Krishan
                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                              LENGTH: 816
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                                               54 EYEIIETIGN 63
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                                                                              3 EIDIIETIGN 12
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8; Conserv
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Tchernev, Velizar
                                                                                                              Conservative
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80.0%;
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    Mişmatches

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Pred. No.
                                                                                                                           Score 40;
Pred. No.
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RESULT 7
US-08-712-072C-4
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; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-328-352-8132
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APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: MUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/
FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 4:
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                   MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 63475/97 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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ORGANISM: gub,
                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bogosian, Elizabeth A. REGISTRATION NUMBER: 39,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: NY
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ADDRESSEE: Ams.....,
ADDRESSEE: Ams....,
ADDRESSEE: Ams...,
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   Rhodothermus marinus
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58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              distein, Alex Zhu and Lin Leng ENDO-BETA-GALACTOSIDASE
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Pred. No.
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61;
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                                                                     Patent No.
                                                                                Sequence 4,
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                               Query Match
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                          GENERAL INFORMATION:
APPLICANT: Kofod,
APPLICANT: Anderse
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Best Local S
                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATION SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/737,526
FILING DATE: 08 NOV-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58719660 No.
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: An Enzyme With Endo-1,3(4)-B-Glucanase TITLE OF INVENTION: Activity
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                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 212 - 655
                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                    Local
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                                                                                                                                                   158 GEIDIMETV 166
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5. 5871966
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                                                                     , Application US/09098580
6140096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 Lexington Avenue
Christgau, Stephan
           Kofod, Lene Venke
Andersen, Lene No. 61400
Kauppinen, Markus Sakari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                       Conservative
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Kauppinen, Markus Sakari
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Pred. No.
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Pred. No.
                        6140096boe
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                                                                                                                                                                                                      Mismatches
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20691
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                                                                                                                                                                                                                                                Sequence 20691, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                   Query Match
                                                                                                            SEQ ID NO 20691
LENGTH: 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
      Matches
                      Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR TILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
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TELEFAX: 212-878-9655
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/737,526
FILING DATE: 08-NOV-1996
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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                    Local Similarity
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Local Similarity 77.8%;
es 7; Conserva++...
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REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
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1998-02-18
                 50.0%;
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               Score 39; DB 4;
Pred. No. 35;
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US-09-330-945-37
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US-08-392-828C-37
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                                                                                    Sequence 37, Appli
Patent No. 6077946
GENERAL INFORMATI
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                                                            APPLICANT:
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APPLICANT:
APPLICANT:
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FILING DATE: .28-FEB-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                  LOCATION: 1..262
OTHER INFORMATION: /note= "BG1 A1 SEQUENCE (FIGURE
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                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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130 SGEIDVMEARG 140
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                                                                                      INFORMATION:
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                                                                                                                                                                                                                                    Similarity 7; Conserv
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SEKI, NOKIAAL
ODA, TOSHIO
ODA, TOSHIO
NA ENCODING HORSESHOE CRAB
                                                            MUTA, TATSUSHI
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SEKI, NORIAKI
                                                                        IWANAGA, SADAAKI
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TITLE OF INVENTION:

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FILING DATE:

11-SEP-1996

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RESULT 13
US-08-712-072C-3
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Best Local
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APPLICANT: Jack Gol.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STREET: NEW YORK
CITY: NEW YORK
CTATE: NY
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                             ADDRESSEE: Ams.....ADDRESSEE: Ams.....
                                             OPERATING SYSTEM: MS-DOS
                                                             COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein LOCATION: 1..262
RRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,072C
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COMPUTER: IBM PC compatible
CPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                      Jack Goldstein, Alex Zhu and Lin Leng
VENTION: ENDO-BETA-GALACTOSIDASE
EQUENCES: 13
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                                                          IBM PC COMPATIBLE
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Pred. No.
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RESULT 14
US-09-092-508-2
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; ORIGINAL SOURCE:
; ORGANISM: e131
US-08-712-072C-3
                                                                              FILING LALE.
CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 60/048,807
APPLICATION NUMBER: 60/055,258
APPLICATION NUMBER: 60/055,258
TTING DATE: 07-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
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TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                  FILING DATE: 07-AUG-1997
ATTORNEY/ACENT INFORMATION:
NAME: Kettelberger, Ph.D., Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 11669.6USU1
                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION MADEER: US/09/092,508 FILING DATE: 05-JUN-1998
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
TELECOMMUNICATION INFORMATION: TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Henzel, William J. TITLE OF INVENTION: APAF-1, P
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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63.6%;
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                                11669.6USU1
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                                                Query Match
Best Local Similarity
"atches 6; Conserv:
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; FRAGMENT TYPE:
US-09-435-115-2
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US-09-435-115-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09435115
Patent No. 6346607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Henzel, William J.

APPLICANT: Henzel, William J.

TITLE OF INVENTION: APAF-1, AN ACTIVATOR OF C ASPASE-3

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSE: Merchant, Gould, Smith, Edell, Welter & Schmidt

STREET: 3100 No. 6346607west Center, 90 South Seventh St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 56.2%;
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/055,258
FILING DATE: 07-AUG-1997
ATTORNEY_AGENT INFORMATION:
NAME: Kettelberger, Ph.D., Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 11669.6USU1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: LBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/435,115
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Minneapolis
                                                                                                                                                                                                                             LENGTH:
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STRANDEDNESS: sir
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Pred. No. 2.9e+02;
4; Mismatches 3; Indels
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Pred. No. 2.9e+02;
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Search completed: September 16, 2003, 11:30:24 Job time: 2.37531 secs

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Perfect score:
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(without alignments)
763.579 Million cell updates/sec
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                                                              A; Molecule type: mRNA
A; Residues: 1-499 <BAC>
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A; Residues: 1-294 <COL>
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                                                                                                                                                                                                                                                                                                          A; Status: preliminary; nucleic
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9; Conserve
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75.0%;
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	57.8	57.8	57.8	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	60.9	60.9	60.9	60.9
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	G97076	T46000	EUSMAG	S73173	T06918	T28301	T45498	в91256	F86096	MMECMK	S75156	A72349	T18265	T48210	AC2850	A97627
	alkaline phosphata	hypothetical prote	agarase (EC 3.2.1.	DNA-directed RNA p	DNA-directed RNA p	ORF MSV140 hypothe	hypothetical prote	inner membrane pro	inner membrane pro	inner membrane pro	hypothetical prote	conserved hypothet	endo-1,3(4)-beta-g	hypothetical prote	GGDEF family prote	hypothetical prote

ALIGNMENTS

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A;Cross-references: GB:U49711; NID:g1488256; PIDN:AAC47235.1; PID:g1488257
A;Accession: PC6037
A;Molecule: type: protein
A;Residues: 21-40;197-209;329-344 <BA2>
A;Experimental source: egg
C;Comment: This enzyme functions in several extracellular activities incluefense enzymes in plants.
C;Keywords: egg; glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                     R;Bachman, E.S.; McClay, D.R.

Proc. Natl. Acad. Sci. U.S.A. 93, 6808-6813, 1996

A;Title: Molecular cloning of the first metazoan beta-1,3

A;Reference number: JC6141; MUID:96270625; PMID:8692900

A;Accession: JC6141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta 1,3-glucanase (EC 3.2.1.-) precursor - sea urchin (Strongylocentrotus purpuratus C;Species: Strongylocentrotus purpuratus (purple urchin) C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 21-Jul-2000 C;Accession: JC6141; PC6037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R,Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gc, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision
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Pred. No. 1.6;
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C;Species: Bacillus circulans
C;Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 31-Mar-2003
C;Accession: JC7869; PC7199
R;Asano, T; Taki, J; Yamamoto, M.; Aono, R.
Biosci. Biotechnol. Biochem. 66, 1246-1255, 2002
A;Title: Cloning and structural analysis of bglM gene coding for the fungal A; Reference number: JC7869; MUID:22152179; PMID:12162545
A;Accession: JC7869
RESULT
E87311
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                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 28-42;95-111;152-170 <AS2>
C;Comment: This protein that is a fungal cell wall-degrading enzyme,
                                                                           B
                                                                                                                                                                                                                      A; Gene:
                                                                                                                                                                                                                                                                                                               A;Cross-references: DDBJ:AB078775
A;Accession: PC7199
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A; Residues: 1-411 < ASA>
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A;Tittle: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
C87296
Celtar-glucanase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001
C;Accession: C87296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell wall-lytic beta-1,3-glucan-hydrolase precursor,
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A; Residues: 1-301 <STO>
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F;21-499/Product:
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8; Conserv
                                                                          SGEIDIMERVNN 156
                                                                                                              SGEIDIIETIGN 12
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ct: beta 1,3-glucanase #status predicted <MAT>
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                                                                                                                                                                 Pred. No. 5
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Pred. No. 2.
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Pred. No.
                                                                                                                                                  Mismatches
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                                                                                                                                                             DB
5.5;
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2.5;
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2.9;
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                                                   ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                       R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.;
                                                                                                                         DNA-directed RNA polymerase beta chain [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: AB2817
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                                A; Authors: Yoo, H.; Tao,
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E.W.

Y.; Biddle,

The

Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58

P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kar

; Chen, L.; Kutyavin, T

T.; Levy, R.; Li,

MCC.

(strain

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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit A;Reference number: AD3252; PMID:11756688
A;Accession: AG3345
                                                                                                                                                                                                                                                               C;Superfamily: DNA-directed RNA polymerase beta chain C;Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1377 < KUR>
A; Cross-references: GB:AE008917; PIDN:AAL51930.1; PID:g17982686; GSPDB:GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Brucella
C;Date: 01-Feb-2002
C;Accession: AG3345
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87311
AB2817
                       RESULT 7
                                                                                                                                                                                                                                                                                                           A; Map position:
                                                                                                                                                                                                                                                                                                                                    A; Gene: BMEI0749
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                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-directed RNA polymerase (EC 2.7.7.6) [imported] - C; Species: Brucella melitensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1356 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: AE005673;
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Best Local S
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8; Conser
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8; Conser
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Pred. No.
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Pred. No.
                                                                                                                                                                        ced. No. 22;
Mismatches
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21;
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A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB2817
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1378 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL42952.1; PID:g1774
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: rpob
A;Map position: circular chromosome
C;Superfamily: DNA-directed RNA polymerase beta chain
                                                                                                                        A; Reference number: Z15794
A; Accession: T06757
A; Molecule type: DNA
A; Residues: 1-736 <QUE>
A; Cross-references: EMBL: ALC
A; Experimental source: culti
C; Genetics:
A; G
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C97595
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C97595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F15B8.180 - Arabidopsis thaliana C;SpecLes: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change C;Accession: T06757
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A;Map position: cir
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A; Molecule type: DNA
A; Residues: 1-1411 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Quetier, F.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, submitted to the Protein Sequence Database, April 1999
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8; Conserv
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             Conservative
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                                                                                                                                                                                                                                                           EMBL:AL049660; GSPDB:GN00061; ATSP:F15B8.180
De: Cultivar Columbia; BAC clone F15B8
                                                                                                                                  208/2; 293/3; 365/3; 384/3; 429/3; 467/3;
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66.7%;
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66.7%;
                                   64.18;
72.78;
      Score 41; DB Pred. No. 25; 1; Mismatches
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RNECB DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Escherichia coli (stra N;Alternate names: transcriptase beta chain C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 31-Oct-1980 #sequence_revision 12-Dec-1997 #text_change 01-Mar-2002 C;Accession: F65205; A91109; JN0244; S12576; A91472; A00689; I52540; I52542;
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R;Zhou, G.; Bao, Z.Q.; Dixon, J.E.
J. Biol. Chem. 270, 12665-12669, 1995
A;Title: Components of a new human protein
A;Reference number: A56708; MOID:95279403;
A;Accession: B56708
                                                                                                                                                                                                                                                                                                           R:Laigret, F.; Gaurivaud, P.; Bove, J.
Gene 171, 95-98, 1996
A;Title: Unique organization of the rpoB region of Spiroplasma A;Reference number: Z22353; MUID:96257200; PMID:8675039
A;Accession: T43730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: ĀTP
F;52-315/Domain: protein kinase homology <KIN>
F;60-68/Region: protein kinase ATP-binding motif
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B56708
                                                                                                                                      C;Superfamily: DNA-directed RNA polymerase beta chain
C;Keywords: nucleotidyltransferase; transcription
                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Spiroplasma citri
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000
C;Accession: T43230
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
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A; Residues: 1-815 <ZHO>
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C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995
                                                                                                                                                                         A; Genetic code:
                                                                                                                                                                                            A; Gene:
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                                                                                                                                                                                                                                                                            A; Molecule type:
                                                                                                                                                                                                                                                                                             A; Status: preliminary;
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I52542;

I52541;

(strain

K-12)

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A; Molecule type: DNA
A; Rolecule type: DNA
A; Residues: 1-105, 'G', 108-383, 'CSRTCSSP' <DEL>
A; Residues: 1-105, 'G', 108-383, 'CSRTCSSP' <DEL>
A; Cross-references: GB: V00341; NID: g42823; PIDN: CAA23629.1;
R; Gurevitch, A.I.; Avakov, A.E.; Kolosov, M.N.
Bloorg. Khim. 5, 1735-1738, 1979
A; Title: The nucleotide sequence at the proximal end of rpoB
A; Title: The nucleotide sequence at the proximal end of rpoB
A; Reference number: A00689
A; Status: significant sequence differences
                     A; Molecule type: DNA
A; Residues: 187-354 <a href="RE2">RE2</a>
A; Cross-references: GB: M38304; NID: 9147719;
R; Gurevich, A.I.; Igoshin, A.V.; Kolosov, M.
Bloorg. Khim. 6, 1580-1584, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 11, 367-373, 1980
A;Title: Nucleotide sequence of the proximal portion of A;Reference number: A91472; MUID:81165543; PMID:7011900
A;Accession: A91472
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Proc. Natl. Acad. Sci. U.S.A. 76, 1697-1701, 1979
A;Title: Nucleotide sequence of the ribosomal protein
A;Reference number: S12572; MUID:79201667; PMID:377281
A;Accession: S12576
                                                                                                                                                          A;Cross-references: GB:M38292; NID:g147717; PIDN:AAA24579.1; PID:g147718 R;Sverdlov, E.D.; Lipkin, V.M.; Monastyrskaya, G.S.; Gubanov, V.V.; Gurye Bloorg. Khim. 6, 309-312, 1980
A;Title: The nucleotide sequence of strong RNA polymerase binding site with A;Reference number: I52542
A;Accession: I52542
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-515,'V',517-1342 <OVC>
A;Residues: 1-515,'V',517-1342 <OVC>
A;Cross references: GB:V00339; GB:J01678; GB:K00449; NID:g42813; PIDN:CAA23625.1;
A;Note: most of this sequence was confirmed by amino acid analysis
A;Note: most of this sequence was confirmed by amino acid analysis
A;Note: most of this sequence was confirmed by amino acid analysis
A;Note: most of this sequence was confirmed by amino acid analysis
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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F65205
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Primary structure of A;Reference number: I52540 A;Accession: I52540
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Bioorg. Khim. 6,
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Gene 11, 367-373,
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A;Reference number: JN0244
A;Accession: JN0244
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A; Title: The primary structure of Escherichia coli RNA polymrase.
A; Reference number: A91109; MUID:81260785; PMID:62668829
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A;Cross-references: GB:AE000472; GB:U00096; NID:g2367333; PIDN:AAC76961.1; PID:g1790419; A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain K-12, substrain MG1655
R;Ovchinnikov, Y.A.; Monastyrskaya, G.S.; Gubanov, V.V.; Guryev, S.O.; Chertov, O.Y.; M
                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-188 <RES>
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A; Residues: 1-33 < POS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G.S.; Gubanov, V.V.; Guryev, S.O.; Lipkin, V.M.; Sverdlov, E.D. 1423-1426, 1980
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Eur. J. Biochem. 177, 363-369, 1988
A;Title: Genes coding for RNA polymerase bet:
A;Reference number: S01794; MUID:89052707; PM
A;Accession: S01794
A;Molecule type: DNA
                                                                                                                                                C;Species: Salmonella typhimurium
C;Date: 31-Dec-1990 #sequence_revision
C;Accession: S01794
R;Lisitsyn, N.A.; Monastyrskaya, G.S.;
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C;Species: Buchnera aphidicola
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-C;Accession: S32680
R;Clark, M.A.; Baumann, L.; Baumann, P.
submitted to the EMBL Data Library, April 1992
A,Description: Sequence analysis of an aphid endosymbiont DNA fragram, Reference number: S32679
A;Accession: S32680
A;Accession: S32680
A;Accession: S32680
A;Residues: 1-1342 <CLA>
A;Residues: 1-1342 <CLA>
A;Cross references: EMBL:Z11913; NID:9296967; PIDN:CAA77970.1; PID C;Superfamily: DNA-directed RNA polymerase beta chain C;Keywords: nucleotidyltransferase; transcription
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A;Map position: 90 min
C;Complex: the active enzyme consists of the sigma c:complex: the active enzyme is composed of two alpha c:punction:
C;Function: part of the catalytic component of C;Superfamily: DNA-directed RNA polymerase beta cf C;Keywords: nucleotidyltransferase; transcription
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A; Residues: 1143-1342 <RE4>
A; Cross-references: GB: M3829
C; Genetics:
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A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Monastyrskaya, G.S.; Gubanov, V
Bioorg. Khim. 6, 1106-1109, 1980
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A; Residues: 1143-1342 <RE3>
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Sverdlov, 31-Dec-1990

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beta

chain -

Salmonella typhimurium

beta subunit in 7; PMID:3056723

bacteria.

Structure/function

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к; науазhi, Т.; Makino, К.; Ohnishi, М.; Kurokawa, К.; Ishii, К.; Yokoyama, К.; Нап, С.G. gasawara, N.; Yasunaga, Т.; Kuhara, S.; Shiba, Т.; Hattori, М.; Shinagawa, Н. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gend A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91242
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F91242
Search completed: September 16, 2003, 11:29:36 Job time: 3.63728 secs
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C;Superfamily: DNA-directed RNA polymerase beta chain
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A;Molecule type: DNA
A;Residues: 1-1342 <HAY>
A;Residues: 1-1342 <HBY>
A;Cross-references: GB:BA000007; PIDN:BAB38333.1; PID:g13364386; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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C;Superfamily: DNA-directed RNA polymerase beta chain
C;Keywords: nucleotidyltransferase; transcription
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C;Species: Escherichia coli
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A;Cross-references: GB:X04642; GB:M37431; GB:X04860; GB:X13854; NID:g47918; PIDN:CAA283
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd
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	1343; lels	se 64	rough he EN restr tent y and isb-s	CH CH CH	C., Silv n F n F PHO:	terobacter	(Transc			P44330 Q105615 Q05615 Q99u25 Q8nwm5 Q8xe4 Q8x14 Q28668 Q02108 P19686 P19686 P19687 P19687
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PRTP_HSVT2

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RESULT
MK07_MC
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Best Local
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MEDIJINE-99319892; PubMed=10392721;

MEDIJINE-99319892; PubMed=10392721;

Bahr U., Springfeld C., Tidona C.A., Darai G.;

Bahr U., Springfeld C., Tidona C.A., Darai G.;

Bahr U., Springfeld C., Tidona C.A., Darai G.;

"Structural organization of a conserved gene cluster of Tupaia

herpesvirus encoding the DNA polymerase, glycoprotein B, a probable processing and transport protein, and the major DNA binding protein.";

Processing and transport protein, and the major DNA binding protein.";

Virus Res. 60:123-136(1999).

-i- FUNCTION: THIS PROTEIN MAY AFFECT TRANSLOCATION OF THE VIRUS

-i- FUNCTION: THIS PROTEIN MAY AFFECT TRANSLOCATION MATURATION
                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitogen-activated protein kinase 7 (EC 2.7.1.-)
regulated kinase 5) (ERK-5) (BMK1 kinase).
MAPK7 OR ERK5.
                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                    MK07_MOUSE
Q9WVS8;
            Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: MEK5 AND ERK5 INTERACT SPECIFICALLY WITH ONE
- NOT WITH MEK1/ERK1 OR MEK2/ERK2 PATHMAYS (BY SIMILARITY
- ENZYME REGULATION: Activated by tyrosine and threonine
                                                                           Kamakura S., Moriguchi T., Nishida E.; "Activation of the protein kinase ERK5/BMK1 | kinases: identification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01366; PRTP;
Capsid assembly.
SEQUENCE 782 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                              Eukaryota; Metazoa; Mammalia; Eutheria;
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Betaherpesvirinae.
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                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                         Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
SIMILARITY: BELONGS TO THE HERPESVIRUSES
                                                                   nucleus."
phosphorylation
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similarity)
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Pred. No.
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A stage;
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                            SIMILARITY)
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; Murinae; Mus
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Best Local
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                                                                                                MK07_HUMAN STANDARD; PRT; 815 AA Q13164; Q16634; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update Mitogen-activated protein kinase 7 (EC 2.7, regulated kinase 5) (ERK-5) (ERK4) (BMK1 ki MAPK7 OR PRKM7 OR ERK5 OR ERK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWART; SM00220; S_TKC; 1.

PROSITE; PS001351; MAPK; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP;

PROSITE; PS00108; PROTEIN_KINASE_DOM;

PROSITE; PS50011; PROTEIN_KINASE_DOM;
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003527; MAP kin
InterPro; IPR000719; Prot_kin
InterPro; IPR002290; Ser_thr
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as lon modified and this statement is not removentities requires a license agreement (Sor send an email to license@isb-sib.ch).
TISSUE-Fetal brain;
MEDLINE-95279403; PubMed-7759517;
Zhou G., Bao Z.Q., Dixon J.E.;
                                NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.
                                                                 Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000001; Prot_kinase; SMART; SM00220; S_TKc: 1
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D; MGI:1346347; 1
; GO:0045765; P::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: THE SECOND PROLINE-RICH REGION MAY INTERACT WITH ACTIN TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL. THE C. AUTOPHORYLATED ON THREONINE AND TYROSINE RESIDUES, WHEN THE C. TERMINAL PART OF THE KINASE, WHICH COULD HAVE A REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROLE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAP KINASE SUBFAMILY
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8; Conserv
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ATP (BY SIMILA
ATP (BY SIMILA
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Pred. No.
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POLY-ARG.
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                                                                    Catarrhini;
                                                                              Craniata; Vertebrata;
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ed. No. 29;
Mismatches
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(EC 2.7.1.-)
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                                                                              Euteleostomi;
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Query Match
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EMBL; U29725; AAA82931.1;
EMBL; U29726; AAA82933.1;
EMBL; U29727; AAA82933.1;
PIR; B56708; B56708.
                                                                                                                    Phosphorylation.
54
DOMAIN 337
DOMAIN 433
DOMAIN 520
DOMAIN 57
NP_BIND 60
BINDING 83
ACT_SITE 181
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J. Biol.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee J.-D., Olevitch R.J., Han J.,

"Primary structure of BMK1: a new mammalian map kinase.";

Biochem. Biophys. Res. Commun. 213:715-724 (1995).

-i- FUNCTION: MEKS AND ERKS INTERACT SPECIFICALLY WITH ONE NOT WITH MEK1/ERK1 OR MEK2/ERK2 PATHWAYS.

-i- ENZYME REGULATION: Activated by tyrosine and threonine
                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                      Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase;
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         GO; GO:0004707; F:MAP kinase activity; GO; GO:0007165; P:signal transduction; InterPro; IPR003527; MAP_kin.
InterPro; IPR007719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphorylation (By similarity).
TISSUE SPECIFICITY: EXPRESSED IN MANY ADULT TISSUES. ABUNDANT IN
HEART, PLACENTA, LUNG, KIDNEY AND SKELETAL MUSCLE. NOT DETECTABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute.
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MAP KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: THE SECOND PROLINE-RICH REGION MAY INTERACT WITH ACTIN TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL. PTM: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE RESIDUES, WHITHE C-TERMINAL PART OF THE KINASE, WHICH COULD HAVE A REGULATOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIVER
                                                                                                                                                                                                                                                       PS00107; PROTEIN_KINASE_ATP; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chem.
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340
464
523
699
68
83
181
218
                                     609
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 62.5%;
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ATP (BY SIM
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POLY-ARG.
                                                           (BY SIMILARITY AREGRTRPHRCLCS
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Length 815;
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                       CRC64
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RESULT 6
RPOB_BUCAI
ID RPOB_BUCAI
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                   HSSP; 09KWU7; 1HQM.
InterPro; IPR001572; RNA_pol_B.
InterPro; IPR001572; RNA_pol_Rpb2_1; 1

Pfam; PF04563; RNA_pol_Rpb2_2; 2.

Pfam; PF04565; RNA_pol_Rpb2_3; 1.

Pfam; PF04565; RNA_pol_Rpb2_7; 1.

Pfam; PF04560; RNA_pol_Rpb2_7; 1.

PR0SITE; PS01166; RNA_POL_BTA; 1.

PR0SITE; PS01166; RNA_POL_BTA; 1.
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P47767;
01-FEB-1996 (
01-FEB-1996 (
15-DEC-1998 (
DNA-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The unique organization of the rpoB region restriction and modification system gene is gene 171:95-98(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-sentities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Mollicutes; Spiroplasmataceae; Spiroplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spiroplasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA' CHAIN.
SIMILARITY: Belongs to the RNA polymerase beta chain family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENZYME WHICH
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                                                                                                                                                                                                                                                                                                                       Transcription;
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. 33, Last sequence update)
. 37, Last annotation update)
. 37, Last annotation (EC 2.7.7.6) (Transcriptase polymerase beta subunit).
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Pred.
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Mismatches
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(See http://www.isb-sib.ch/announce/
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RESULT 7
RPOB_BUCAP
ID RPOB_B
AC P41184
AC P41184
DT 01-FEB
DT 28-FEB
DE DNA-d1.
DE beta c1.
GN RPOB 00
OS Buchne
OC Bacter
OC Enterol
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Best Local S
Matches 7
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HSSP; Q9KW17; 1HQM.
InterPro; IPR001572; RNA_pol_B.
Pfam; PF04563; RNA_pol_Rpb2_1; 1.
Pfam; PF04561; RNA_pol_Rpb2_2; 1.
Pfam; PF04565; RNA_pol_Rpb2_3; 1.
Pfam; PF04565; RNA_pol_Rpb2_6; 1.
Pfam; PF00562; RNA_pol_Rpb2_7; 1.
Pfam; PF04560; RNA_pol_Rpb2_7; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
                                                         RPOB_BUCAP
P41184;
01-FEB-1995
01-FEB-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM 198;
STRAIN=TOKYO 1998;
MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M.,
Shigenobu S., Watanabe H., Hattori M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P57146;
16-OCT-2001
16-OCT-2001
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Nature 407:81-86(2000).

-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCH-
--- FUNCTION: DNA-DEPENDENT RNA POLYMERASE THE TRANSCH-
--- FUNCTION: DNA-DEPENDENT RNA POLYMERASE THE POLYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.)
beta chain (RNA polymerase beta subunit).
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Enterobacteriaceae; Buchne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                symbiotic bacterium).
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SUBUNIT: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate
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           Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buchnera
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                                                Schizaphis graminum)
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Pred. No.
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3; Mismatches
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RESULT 8
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Best Local
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HSSP; O9KWU7; 1HOM.
InterPro; IPRO01572; RNA_pol_B.
Pfam; PF04563; RNA_pol_Rpb2_1; 1
Pfam; PF04561; RNA_pol_Rpb2_2; 1
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Pfam; PF04565; RNA_pol_Rpb2_3; 1.
Pfam; PF00562; RNA_pol_Rpb2_6; 1.
Pfam; PF04560; RNA_pol_Rpb2_7; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
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PIR;
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                                              Escherichia coli 06,
Escherichia coli 0157:H7,
                                                                     Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-slb.ch).
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MEDLINE=93160925; PubMed=1369199;
Clark M.A., Baumann L., Baumann E
                       Shigella
                                                                                                  Escherichia coli,
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SPECIES-E.coli; STRAIN=0157:H7 / EDL933 / ATCC 7009Z/;

MEDLINE-21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatril Posfai G., Hackett J., Kilnk S., Boutin A., Shao Y., Mil Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potam Standard J., Anantharaman T.S., Lin J., Yen G., Schwartz
                                                                                                                                                                                               SEQUENCE FROM N.A.

SPECIES-E.coli; STRAIN=0157:H7 / RIMD 0509952;

MEDLINE-21156231; PubMed=11258796;

MEDLINE-21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T. Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-E. col1; STRAIN-06:H1 / CFT073 / ATCC 700928; MEDLINE-22388234; PubMed-124711157; Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mohley H.L.T., Donnenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome of uropathogenic Escherichia coli."; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
SEQUENCE OF 1-391
SPECIES-E.coli;
MEDLINE-81165543;
                                                                                                                                                                                                                                                                                                                                                        Nature
[6]
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SPECIES-E.coli; STRAIN-B;
Miller E.S., Shih G.C., Chung
chamitted (NOV-1996) to the Ex
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Ovchinnikov Y.A., Monastyrskaya G.S., Gubanov V.V., Guryev S.O.,
Chertov O.Y., Modyanov N.N., Grinkevich V.A., Makarova I.A.,
Marchenko T.V., Polovnikova I.N., Lipkin V.M., Sverdlov E.D.;
"The primary structure of Escherichia coli RNA polymerase. Nucleotide sequence of the rpoB gene and amino-acid sequence of the
                                                                                                                                                                              [7]
                                                                                                                                                                                                                                                                                                                                                                      Apodaca J., Anantharaman T.S., Lin J., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Nature 409:529-533(2001).
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SPECIES-E.coli; STRAIN-K12 / MG1655;
MEDLINE-94089392; PubMed-8265357;
Belatiner F.R., Burland V.D., Plunket
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                                                             Post L.E., Strycharz G.D., Nomura M., Lewis H., "Nucleotide sequence of the ribosomal protein ge to the gene for RNA polymerase subunit beta in E Proc. Natl. Acad. Sci. U.S.A. 76:1697-1701(1979)
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8:11-22(2001).
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hao Y., Miller L.,
E.T., Potamousis K.,
, Schwartz D.C.,
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SPECIAL Syerdlov E.D., Lipki... Syerdlov E.D., Chertov O.Y.; Guryev S.O., Chertov O.Y.; "The nucleotide sequence of strong RY the E.coli rpoB structural gene."; "increa. Khim. 6:309-312(1980).
                                                                                                                                                                                                                                                                                                                                           Gurevich A.I., In "Structure of a sequence of the Bioorg, Khim. 6:
                                                                                                                        "Genome :
through :
Nucleic :
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"A beta subunit mutation disrupting the catalytic function of Escherichia coli RNA polymerase.",

Proc. Natl. Acad. Sci. U.S.A. 88:6018-6022(1991).

-j- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                   MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y.,
Yang J., Yang F., Zhang X., Zhang J., Yar
Sun L., Xue Y., Zhao A., Gao Y., Zhu J.,
Cheng H., Yao Z., He B., Chen R., Ma D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Primary structure of RNA polymerase from of the rpoB gene fragment and correspondin sequence of the beta-subunit."; . Bioorg. Khim. 6:1423-1426(1980).
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                                                                      MEDLINE=91296752; PubMed=2068078;
                                                                                                                                                                                                                                                                     Mollet C., Drancourt M., Raoult "RNA polymerase beta-subunit."; Submitted (NOV-1996) to the EMBI
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                                                                                                                                                           Yu J.;
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                                                                                                                        nce of Shigella flexneri rison with genomes of Esc. Res. 30:4432-4441(2002).
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6:1580-1584(1980).
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Escherichia coli K12
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J., Kan B.,
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B., Ding K., Chen S.,
g B., Wen Y., Hou Y.,
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SWISS-2DPAGE; P00575; COLI.
ECOZDBASE; D157.0; 6TH EDITION.
ECOGENE; EG10894; rpoB.
InterPro; IPR001572; RNA_pol_B.
                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium.
Bacteria; Proteobacteria;
Enterobacteriaceae; Salmor
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          SEQUENCE FROM N.A. MEDLINE-89052707;
                                                                                                Sverdlov E.D., Lisitsyn N.A., Guryev S.O., "Nucleotide sequence of the rpoB gene of s. for the beta-subunit of RNA polymerase.";
Dokl. Biochem. 287:62-65(1986).
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GEL; W76222; AAB18647.1; -.
GEL; M76222; AAB18647.1; -.
GEL; AE016770; AAN83372.1; ALT_INIT.
GEL; AE005630; AAG59183.1; -.
GEL; W00341; CAA23629.1; -.
GEL; W00341; CAA23629.1; -.
GEL; M38292; AAA24579.1; -.
GEL; M38292; AAA24580.1; -.
GEL; M38293; AAA24580.1; -.
GEL; M38287; AAA24581.1; -.
GEL; M38293; AAA24581.1; -.
GEL; M38303; AAA24581.1; -.
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2 ALPHA CHAINS, 1 BETA CHAIN,
                                                                                                                                                                ., Monastyrskaya G.S.;
Samonella typhimurium
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InterPro; IPR001572; RNA_pol_B.
Pfam; PP044563; RNA_pol_Rpb2_1; 1
Pfam; PF04561; RNA_pol_Rpb2_2; 1
Pfam; PF04565; RNA_pol_Rpb2_3; 1
Pfam; PF00562; RNA_pol_Rpb2_5; 1
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CONFLICT
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typhimurium gene rpob.";
Bioorg, Khim, 12:699-707(1986).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
--- TO THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 187-1144 FROM N.A.
MEDLINE-86269165; PubMed-3019156;
Sverdlov E.D., Lisitsyn N.A., Guryev S.O., Smirnov Y.V.,
Rostapshov V.M., Monastyrskaya G.S.;
"Genes encoding the beta-subunit of bacterial RNA-polymerases.
Primary structure of the EcoRI-C fragment of the Salmonella
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Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S.
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., will
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                            PIR;
                                                                                                                                                                                                                                                                                                       EMBL; X04642; CAA28302.1; --
EMBL; AF170176; AAF23499.1; --
EMBL; AE008894; AAL22981.1; --
EMBL; M38311; AAA27215.1; --
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Eur. J. Biochem. 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence LT2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isitsyn N.A., Monastyrskaya G.S., Sve
"Genes coding for RNA polymerase beta
Structure/function analysis.";
Eur. J. Biochem. 177.:363-369(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lisitsyn N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, I BETA CHETA' CHAIN.

SIMILARITY: Belongs to the RNA polymerase beta chair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC
                                                                                                                                                                                                                                                                             S01794; RNEBBT.
440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA)(N).
                        N
                                                   Similarity
7; Conser
                                                                                                                                                                        PS01166; RNA_POL_BETA;
GEVDDIDHLGNR
                                                                                                                                           proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF,
                          GEIDIIETIGNR
                                                                                                      401
542
1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187-1144 FROM N
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Bioinformatics Institute. The profit institutions as long
                                                                                                                                                         Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                       A,
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542
; 150600
                                                               62.5%;
58.3%;
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451
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R R G
                                                                                                                                                          DNA-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enterica
                                                   Pred. No. 48;
; Mismatches
                                                                          Score 40;
                                                                                                                   > A (IN REF. 4).
> L (IN REF. 1, 2
8143964BF1709C02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sverdlov E.
eta subunit
                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                            DB
48;
                                                                                                                                                                                                                                                                                                                                                                                                                          There
                                                                                                                                                          RNA
                                                                                                                                                                                                                                                                                                                                                                                                             as its content
                                                                             1;
                                                                                                                                                          polymerase;
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                                                 2:
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                                                                             Length 1342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             serovar Typhimurium
                                                                                                      AND 4)
CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain family.
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                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Latreille P., Du S., Layman D., Mulvaney E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN,
                                                                                                                                                                                                                                                                                                                                                                                                   and
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RESULT 11
RPOB_VIBCH
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Best Loc
Matches
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Pfam; PF04563; RNA_pol_Rpb2_1; 1.
Pfam; PF04565; RNA_pol_Rpb2_2; 1.
Pfam; PF04565; RNA_pol_Rpb2_3; 1.
Pfam; PF00562; RNA_pol_Rpb2_6; 1.
Pfam; PF04560; RNA_pol_Rpb2_7; 1.
Pfam; PF04560; RNA_POL_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields A., Godayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Weidman J.F., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPOB_HAEIN STANDARD; PRT; 1343 AA. P43738; O1-NOV-1995 (Rel. 32, Created) O1-NOV-1995 (Rel. 32, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) DNA-directed RNA polymerase beta chain (EC 2.7.7.6) beta chain) (RNA polymerase beta subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
Science 269:496-512(1995).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
MEDLINE-95350630; PubMed 7542800;
                                                                                                                                                                                                                          Transferase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
Pasteurellaceae; Haemophil
NCBI_TaxID=727;
[1]
                                                                                                                                                                                                                                                                                                                                                              TIGR;
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U32733; AAC22173.1; -. PIR; H64073; H64073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae
                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: N nucleoside triphosphate =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RNA)(N).
SUBUNIT: THE ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENZYME WHICH IS
                                                                                                                                                                                                                                                                                                                                                            Q9KWU7; 1HQM.
HI0515; -.
                                                                440
                                                                                                N
                                                                                                                              Similarity 7; Conser
                                                                                              GEIDIIETIGNR 13
                                                                                                                                                                                                            proteome
                                                                GEVDDIDHLGNR 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN.
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                                                                                                                                              62.5%;
58.3%;
                                                                                                                                                                                               149783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                               ¥;
                                                                                                                           Score 40; DB
Pred. No. 48;
3; Mismatches
                                                                                                                                                                                                                            DNA-directed RNA polymerase;
                                                                                                                             ű
                                                                                                                                                                                             4EF99CD648686A44 CRC64;
                                                                                                                                         DB
48;
                                                                                                                             2;
                                                                                                                                                             Length 1343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BETA CHAIN,
                                                                                                                             Indels
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RESULT 12
RPOB_NEIMA
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Best Local S
Matches 7
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Pfam; PF04563; RNA_pol_Rpb2_1; 1.
Pfam; PF04561; RNA_pol_Rpb2_2; 1.
Pfam; PF04565; RNA_pol_Rpb2_3; 1.
Pfam; PF00562; RNA_pol_Rpb2_6; 1.
Pfam; PF04560; RNA_pol_Rpb2_7; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
RPOB_NEIMA STANDARD;
P57009;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-El Tor N16961 / Serotype 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelln H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000).

-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES (By Similarity).

-i- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit).
                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 1375 A/
                                                                                                                                                                                                                                                                                       Transferase; Transcription; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE004121; AAF93501.1; -. PIR; F82336; F82336.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salzberg S.L., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPOB OR VC0328.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RNA)(N).

SUBGNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND BETA' CHAIN (By similarity).

SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                      474
                                                                                                                                                                                                                                                                                                                                                                                                                       Q9KWU7; 1HQM.
VC0328; -.
                                                                                                                                                      N
                                                                                                                                                                                     Similarity 7; Conserv
                                                                                                                      GEVDDIDHLGNR
                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                        AA; 153285 MW;
                                                                                                                                                                                                       62.5%;
58.3%;
                                                                                                                      485
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                                                                                                                                                                                                       Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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RESULT 13
RPOB_N
RPOB_N
ID RPOB_N
AC Q59672
DT 16-OCT
DT 16-OCT
DE DNA-d1
DE beta c
GN RPOB o
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Best Local S
Matches 7
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InterPro; IPR001572; RNA_pol_B.
Pfam; PF04563; RNA_pol_Rpb2_1; 1.
Pfam; PF04561; RNA_pol_Rpb2_2; 2.
Pfam; PF04565; RNA_pol_Rpb2_3; 1.
Pfam; PF04566; RNA_pol_Rpb2_6; 1.
Pfam; PF04560; RNA_pol_Rpb2_7; 1.
Pfam; PF04560; RNA_pol_Rpb2_7; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
                                                    RPOB_NEIMB
Q59622;
Q1-NOV-1997
16-OCT-2001
16-OCT-2001
       01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.
beta chain) (RNA polymerase beta subunit).
RPOB OR NMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatic
the European Bioinformatics Institute. Ther
use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See borsend an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quall M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-directed RNA beta chain) (RNA RPOB OR NMA0142.
                                                                                                                                                                                                                                                                                                                            Transferase; Transcription; DNA-directed RNA polymerase; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Z2491 / Serogroup A / Serotype
MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis (serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENZYME WHICH IS COMPOSED OF BETA' CHAIN.
SIMILARITY: Belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {RNA}(N).
SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CONSISTME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBSTRATES.
CATALYTIC ACTIVITY: N nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              D82007; D82007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL162752; CAB83457.1;
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                                                                                                                                                                                                                                                    7; Conserv
                                                                                                                                                                                           GEVDDIDHLGNR
                                                                                                                                                                                                                  GEIDIIETIGNR
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                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                    62.5%;
58.3%;
                                                                                                                                                                                           478
                                                                                                                                                                                                                        13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         annotation update)
e beta chain (EC 2.7.7.6)
e beta subunit).
                                                                                                                                                                                                                                                 Score 40; DB Pred. No. 50; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                             BA4AF438619CB82C CRC64;
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                                 2.7.7.6) (Transcriptase
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HSSP, Q80007; 1100.

TIGR; NMB0132; --

InterFO; IPR001572; RNA_pol_B.

Pfam; PF04563; RNA_pol_Rpb2_2; 2.

Pfam; PF04561; RNA_pol_Rpb2_2; 2.

Pfam; PF04565; RNA_pol_Rpb2_3; 1.

Pfam; PF04562; RNA_pol_Rpb2_6; 1.

Pfam; PF04560; RNA_pol_Rpb2_6; 1.

Pfam; PF04560; RNA_pol_Rpb2_6; 1.
                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B. Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E. Cotton M.D., Utterback T.R., Khourl H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B s
                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 287:1809-1815(2000).
-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=MC58 / Serogroup
MEDLINE=20175755; PubMee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome MC58.";
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Submitted (OCT-1995)
                                                                                                                                                                                                                                                 Transferase;
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Bacteria; Proteobacteria; Betaproteobacteria;
                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBSTRATES.

CATALYTIC ACTIVITY: N nucleoside triphosphate = {RNA}(N).

SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN SUBUNIT: THE ENZYME COMPOSED OF 2 ALPHA CHAINS, 1 BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BETA' CHAIN. SIMILARITY: Belongs to the RNA polymerase beta chain family
                                                                                                                                                                                                                                                                                                                                                                                   ; AE002371; AAF40591.1; ALT_INIT.
T30824; T30824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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/ Serogroup
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ders N.J., Heidelberg
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GG -> A (IN REF. 1).
F -> L (IN REF. 1).
GY -> VN (IN REF. 1).
YNG -> SR (IN REF. 1).
                                                                                                                                                                                                                                               DNA-directed RNA polymerase;
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ILDIFYDKETFYLSSNGVQTDLVADRLKG
                                                                                                         MISSING (IN REF. 1)
A -> G (IN REF. 1).
A -> P (IN REF. 1).
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N -> L (IN REF. 1).
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2 ALPHA CHAINS, 1 BETA CHAIN,
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SR (IN REF. 1).
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Matches 7
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MEDLINE-96095775; Pubmed-852578;
Altchison J.D., Rout M.P., Marelli M., Blobel G., Wozniak R.W.;
"Two novel related yeast nucleoporins Nupl70p and Nupl57p:
complementation with the vertebrate homologue Nupl55p and funct
                                                                                                                                                                                                                                                                                                                                                                                                                                   Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Jagels K., Lye G., Moule S., Odell C., Pearson D., Raja Rice P., Skelton J., Walsh S., Whitehead S., Barrell B. "The nucleotide sequence of Saccharomyces cerevisiae ch
                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                   Interactions with the yeast nuclear pore-membrane prote
J. Cell Biol. 131:1133:1148(1995).
I. FUNCTION: INTERACTS WITH THE CORE STRUCTURE OF THE
COMPLEX (NPC). MAY PROVIDE THE NECESSARY ASYMMETRY
ANCHORING STRUCTURES SUCH AS CYTOPLASMIC FILAMENTS
NUCLEDOPLASMIC CAGE
I. SUBUNIT: INTERACTS WITH NUP170 AND/OR POM152.
I. SUBCELLULAR LOCATION: Nuclear pore complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat Nucleoporin NUP188 (Nuclear pore protein NU NUP188 OR YML103C.
                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=9169872;
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Nehrbass U., Rout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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 S47446; S47446.

$ $0004571; NUP188.

GO:0005643; C:nuclear

GO:0006999; P:nuclear
                                                      X90580; CAA62208.1;
U47107; AAA88904.1;
X80835; CAA56794.1;
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7; Conserv
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1 (JAN-1996)
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58.3%;
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pore; IDA.
pore organization
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e EMBL/GenBank/DDBJ
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             cerevisiae chromosome
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biogenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rajandream
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the companies of the companies o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spilliaert R., Hreggvidsson G.O., Kristjan
Eggertsson G., Palsdottir A.;
"Cloning and sequencing of a Rhodothermus
for a thermostable beta-glucanase and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GUB_RHOMR STANDARD; PRT; 286 AA. P45798; P45798; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                      PIR; S48201; S4820
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U04836; AAA60459.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-21 / ITI-378;
                                                                                                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95010084; PubMed=7925416;
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Bacteria; Bacteroidetes; Sphingobacteria; Sph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crenotrichaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. BIOChem. 224:923-930(1994).

FUNCTION: SHOWS ACTIVITY ON LICHENAN, BETA-GLUCAN AND LAMINARIN BUT NOT ON CMC CELLULOSE OR XYLAN.

CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.

MISCELLANEOUS: The enzyme has a temperature optimum of 85 degree: Celsius and a pH optimum of 7.0.

SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
      156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1290 SGEIDFIKNIG 1300
                                                                                                                                                                                                                                                                                                  PF00722; Glyco_hydro_16; 1.
TE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                       Similarity 7; Conser
:|||||:|:|
NGEIDIMEHVG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
8; Conserv
                                             SCEIDIIETIG
                                                                                                                                                                                                                                                                                                                                               IPR000757; Glyco_hydro_16.
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                                                                                                                                                                      31
158
163
286
                                                                                                                                                                                                                                                                                  Glycosidase;
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                                                                                                                                                                                                                                                                                  Signal.
                                                                                                                                                                           W.
                                                                                                         Score 39;
Pred. No.
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                                                                                                                                                                      BETA-GLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY);
7215C33624135191 CRC64;
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Pred. No.
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Search completed: September 16, 2003, 11:26:28 Job time : 1.91688 secs

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Result
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Q9ab54 caulobacter
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   068641 oerskovia x
Q8gcz7 lysobacter
Q96tu5 alternaria
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                                                                  SGEIDIIETIGNR 13
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ALIGNMENTS

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RESULT
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O77072 PRELIMINARY; PRT; O77072; O1-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Beschin A., De Baetselier P., Bilej M.;

Beschin A. De Baetselier P., Bilej M.;

"Distinct carbohydrate recognition domains of an earthworm defense molecule recognize Gram negative and Gram positive bacteria.";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

SMBL; AF395805; AAL09587:1;

InterPro; IPR000757; Glyco_hydro_16.

Pfam; PF00722; Glyco_hydro_16; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Coelomic cytolytic factor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lumbricus terrestris (Common earthworm).
Eukaryota: Metazoa: Annelida; Clitellata; Oligochaeta; Haplotaxida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lumbricina; Lumbricidae; Lumbricus.
                                                                                                                                                        SGEIDIIETIGNR 190
                                                                                                                                                                                                                                                                                                                              43931 MW;
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; 5256CF171EB7D3FB CRC64;
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Pred. No. 0.0023;
Mismatches 0
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RA Beschin A., Bilej M., Hanssens F., Raymakers J., Van Dyck E.,

RA Revets H., Brys L., Gomez J., De Baetseller P., Timmermans M.;

RT "Identification and cloning of a glucan- and Lipopolysaccharide-

RT binding protein from Eisenia foetida earthworm involved in the

RT activation of prophenoloxidase cascade.";

RL J. Biol. Chem. 273:24948-24954(1998).

DR EMBL; AF030028; AA035887.1; -

DR InterPro; IPR000757; Glyco_hydro_16.

DR Pfam; PF00722; Glyco_hydro_16; 1.

"C SCOURGE 384 AA; 44322 MW; C90B5C94003BAD6D CRC64;

"C SCOURGE STANDARD ST
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Q51333;
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96345651; PubMed-8755914; Ferrer P., Halkier T., Hedegaard L., Savva D., Diers I., Asenjo J.A.; "Nucleotide sequence of a beta-1,3-glucanase isoenzyme IIa gene of Oerskovia xanthineolytica LL G109 (Cellulomonas cellulans) and initial characterization of the recombinant enzyme expressed in Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998
01-OCT-2001
         Q900G4
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EMBL; U56935; AAC44371.1; -.

HSSP; P23904; 1AATK.

InterPro; IPR000757; Glyco_hydro_16.

Pfam; PF00722; Glyco_hydro_16; 1.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.

SEQUENCE 306 AA; 32835 MW; CD8DB8C1A6)
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NCBI_TaxID=1710;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Promicromonosporaceae; Cellulosimicrobium.
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01-OCT-2002 (TremBI
Beta-1,3-glucanase
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Lumbricina;
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Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
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NCBI_TaxID=6396;
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             PRELIMINARY;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                     Score 50;
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Pred. No.
             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                   CD8DB8ClA6F8DC04 CRC64;
                                                                                                                                                                                                                                                                                           Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation updat
r;nonolvsaccharide and beta-1,3-glucan binding pr
                                                                                         "Toward the sialome of the adult female mosqui submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AF466594; AAL76017.1; -... IPR000757; Glyco_hydro_16. ffam; PF00722; Glyco_hydro_16; 1. SEQUENCE 371 AA; 41943 MW; IFE2E5DC7B665CE
                                                                                                                                                                                                                                    Putative secreted protein.
Aedes aegypti (Yellowfever mosquito).
Eukaryota, Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Nematocera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         purification, characterization, and cDNA cloning.";
J. Biol. Chem. 275:1337-1343(2000).
EMBL; AJZ50128; CAB65353.1;
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=20092910; PubMed=10625682;
Lee S., Wang R., Soderhall K.;
"A lipopolysaccharide- and beta-1,3-glucan-binding protein from hemocytes of the freshwater crayfish Pacifastacus leniusculu:
                                                                                                                                                              STRAIN-Black eye; TIS: Valenzuela J.G., Pham Ribeiro J.M.C.;
                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eumalacostraca; Eucario
Astacoidea; Astacidae;
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Eukaryota; Metazoa; Arthropoda; Crustacea;
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                                                                                                                                                                                                                         NCBI_TaxID=7159;
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                                               Conservative
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acidae; Pacifastacus
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Pham V.M., Garfield M.K.,
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361
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75.0%;
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 211
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                                             Score 47; DB
Pred. No. 3.1;
4; Mismatches
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Pred. No.
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; 93A5E67911ED6619 CRC64;
                                                                                           1FE2E5DC7B665CE6
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era; Culicoidea; Aed
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                                                                                            CRC64;
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Submitted (APR-2001) to the EMBL/GenBa EMBL; AF368168; AAM21213.1;
Interpro; IPR000757; Glyco_hydro_16; 1.
SEQUENCE 366 AA; 41497 MW; 6F540A6
    007242
007242;
01-JUL-1997
01-JUL-1997
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OBNON3;
OBNON3;
O1-OCT-2002 (TrEMBLrel. 2
O1-OCT-2002 (TrEMBLrel. 2
O1-MAR-2003 (TrEMBLrel. 2
D1-MAR-2003 (TrEMBLrel. 2
Beta-1,3-91ucan binding penaeus monodon (Penoeid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Hepatopancreas;
TISSUE-Hepatopancreas;
MEDLINE-22068042; PubMed-12072514;
Roux M.M., Pain A., Klimpel K.R., Dhar A.K.;
The Lipopolysaccharide and beta-1,3-Glucan Binding Protein
The Lipopolysaccharide and beta-1,6-Glucan Binding Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Lipopolysaccharide and beta-1,3-glucan binding protein.
Litopenaeus stylirostris (blue shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Peraeddae; Litopenaeus.
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Penaeus monodon (Penoeid shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
Penaeddae; Penaeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=29019;
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Pro; IPR000757; Glyco_hydro_16.
PF00722; Glyco_hydro_16; 1.
PF00723; Glyco_hydro_16; 1.
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  (TrEMBLrel.
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                                                                       PRELIMINARY;
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binding
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75.0%;
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75.0%;
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ding protein from th
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Last sequence update)
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Pred. No. 4.7;
                                                                    PRT;
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D7ADC5A310208885 CRC64;
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6F540A60E83FDD7D CRC64;
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy A. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
T "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
N 121 Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; Wr0329; -.
TIGR; Wr0329; -.
TubercuList; Rv0315; -
InterPro; IPR006311;
InterPro; IPR006311;
                                                                                                                                             01-JUN-2001
01-JUN-2001
01-OCT-2001
                  SEQUENCE FROM N.A. Schulte U., Aign V., Nyakatura G., Mewes
                                                                Neurospora crassa.

Eukaryota; Fung1; Ascomycota; Pezizomycotina;

Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID-5141;
                                                                                                                                                                                                                                                                                                                                                                                Complete CONFLICT
                                                                                                                        B7A16.110.
                                                                                                                                    Related
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InterPro; IPR006311; Tat.
Pfam; PF00722; Glyco_hydro_16; 1.
TIGRPAMS; TIGR01409; TAT_signal_seq; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2001) to the EMBL; Z96800; CAB09586.1; -. EMBL; AE006940; AAK44553.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peterson J., DeBoy R., Dodson Kolonay J.F., Nelson W.C., Uma Delcher A., Utterback T., Weicher
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Corynebacterineae; Mycobacteriaceae;
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294 AA;
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W.C., Umayam L.A., Ermolaeva
T., Weldman J., Khouri H., (
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     isel J., Brandt P., I
Mannhaupt G.;
he EMBL/GenBank/DDBJ
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n binding protein.
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Pred. No. 5.6;
1; Mismatches
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va M., Salzberg ;
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K MEDLINE-96270625; PubMed-8692900;

A Bachman E.S., McClay D.R.;

T "Molecular cloning of the first metazoan beta-1,3 gluver of the sea urchin Strongylocentrotus purpuratus.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:6808-6813(1996).

DR EMBL; U49711; AAC47235.1; -.

DR EMBL; U49711; AAC47235.1; -.

DR EMBL; U49711; AAC47235.1; -.

T.ENGTENDER 499 AA; 55275 MW; D863F36EE0CFF5AC CRC6
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German Neurospora genome project;
Submitted (FEB-2001) to the EMBL/GenBa
EMBL; AL513445; CAC28724.1; -.

InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.

SEQUENCE 462 AA; 51868 MW; 28808B6
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01-NOV-1996 (TremBLr
01-DEC-2001 (TremBLr
Beta 1,3-glucanase
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Q9AB54;
Q1-JUN-2001
01-JUN-2001
01-MAR-2002
 STRAIN-ATCC 19089 / CB15;

MEDLINE-21173698; PubMed-11259647;

Micrman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.
Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., E
Potocka I., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Wh
                                                                                                                     Bacteria; Proteobacteria; Alpl
Caulobacteraceae; Caulobacter
NCBI_TaxID=155892;
                                                                                                                                              Caulobacter crescentus
Bacteria; Proteobacter
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinocea; Echinoida; Strongylocentrotidae;
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Q26660;
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NCBI_TaxID=7668;
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01-MAR-2001
01-MAR-2003
                                                     coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL939106; CAC14352.1;
                                                                                                                                       STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil
InterPro; IPR000757; Glyco_hydro_16.
InterPro; IPR000772; Ricin_B_lectin.
Pfam; PF00722; Glyco_hydro_16; 1.
Pfam; PF00652; Ricin_B_lectin; 3.
                                                                                                          Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                             HSSP;
                                                                                    "Complete genome
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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Cerdeno A.M.,
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SEQUENCE
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                                                                                                                                                                                                                                                              Kinashi H., Hopwood D.A.;
"A set of ordered cosmids
                                                                                                                                                                                                                                                                                   Redenbach M.,
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NCBI_TaxID=1902;
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Pfam; PF00722; Glyco_hydro_16; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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Streptomyces coelicolor
robiol. 21:77-96(1996).
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r A3(2) chromosome
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Best Local
                                                                                         HSSP: P23904; 1AJK:
InterPro; IPR000757; Glyco_hydro_16.
InterPro; IPR000772; Ricin_B_lectin.
Pfam; PF00722; Glyco_hydro_16; 1.
Pfam; PF00552; Ricin_B_lectin; 3.
SMART; SM00458; RICIN; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
PROSITE; PS0231; RICIN_B_LECTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.....
STRAIN-LL G109;
STRAIN-LL G109;
MEDLINE-96250169; PubMed-8659924;
MEDLINE-96250169; PubMed-8659924;
Ferrer P., Hedegaard L., Halkler T., Diers I., Sar
Perrer P., Hedegaard L., Halkler T., Diers I., Sar
Molecular cloning of a lytic beta-1,3-glucanase
xanthineolytica LL G109.";
xanthineolytica LL G109.";
y. Acad. Sci. 782:555-566(1996).
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068641;
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Bacteria; Actinobacteria; Actinobacteri
Micrococcineae; Promicromonosporaceae;
                                                                                                                                                                                                                                                                                   Submitted (MAR-1998) to the EMBL; AF052745; AAC38290.1;
                                                                                                                                                                                                                                                                                                                               "BglII codes for a yeast-lytic beta-1,3-glucanase from Oerskovia xanthineolytica LL G109 (Cellulomonas cellulans) having a mannoss binding domain.";
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PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
PROSITE; PS50231; RICIN_B_LECTIN; 1.
Hydrolase; Complete proteome.
SEQUENCE 422 AA; 44143 MW; 71050471
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-LL G109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular characterisation of a thermoactive Oerskovia xanthineolytica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parrado J., Escuredo P.R.,
Asenjo J.A., Dobson C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96409238; PubMed=8814220;
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68.8%;
72.7%;
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Last annotation update)
Score 44;
Pred. No.
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SEQUENCE
                                                                                                                                         Eshel D., Prusky D., Dinoor A.;
"Mixed-linked glucanase precursor of Alternaria alternat Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF282319; AAK69516.1; -
                                                                                                                                                                                                             Mixed-linked glucanase (Fragment).
Alternaria alternata.
Alternaria alternata.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporates; Pleosporaceae; mitosporic Pleosporaceae; Alterna NCBI_TaxID-5599;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Palumbo J.D., Sullivan R.F., Kobayashi D.Y.; "Molecular characterization of three beta-1,3-glucanase ge Lysobacter enzymogenes strain N4-7 and partial biochemical characterization of their gene products by expression in
                                                                                                                                                                                                                                                                                                                   Q96TU5
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Bacteria; Proteobacteria;
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LA; 31073 MW;
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Search completed: September 16, 2003, 11:28:40 Job time : 7.99496 secs

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Copyright (c) 1993 - 2003 Compugen Ltd
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                 Eisenia foetida co
Drosophila melanog
Oerskovia xanthine
Oerskovia xanthine
Oerskovia xanthine
Bombyx mori mature
Bombyx mori full 1
Beta-1,3-glucanase
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Bacillus circulans
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Herbicidally activ	Arabidopsis thalia	Listeria monocytog	٠.			₽.		Haemophilus influe	n me	Gene 21 human secr	Cytophaga drobachi	⋖	Arabidopsis thalia	_	Κ.		Arabidopsis thalia	A.altocetigenes me	R flavefaciens xyl	Ruminococcus flave	ADH complex protei	Bankia qouldi endo	Bifidobacterium lo	Phaffia rhodozyma	Trichoderma harzia	vcobacterium tub	Streptomyces sp. S	str ·	3)-beta		≡e	mela	Ė	a melano	Oerskovia beta-1,3	

ALIGNMENTS

RESULT 1 AAY24914

AAY24914 standard; Protein;

384 AA

AAY24914;

(VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG 17-DEC-1997; 16-DEC-1998; 24-JUN-1999 WO9931229-A2 Protein Key Eisenia foetida. Peptide 97EP-0203974. 98WO-EP08169 /label= signal 18..384 Location/Qualifiers /label= CCF-1

Eisenia foetida; coelomic cytolytic factor 1; CCF-1; cancer; trypanosomal infection; bacterial infection; tumour therapy; inflammation; immunology.

Eisenia foetida coelomic cytolytic factor 1 protein.

25-AUG-1999 (first entry)

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RESULT 2
ABB62773
ID ABB6
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AC ABB6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 384; Conserv
pharmaceutical.
           Drosophila; developmental
                                     Drosophila melanogaster polypeptide SEQ ID NO 15111.
                                                                   26-MAR-2002
                                                                                               ABB62773;
                                                                                                                         ABB62773 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       foetida polypeptides derived
                                                                                                                                                                                               GAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW
                                                                                                                                                                                                                                                                                                                                                                                        IDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GANSFYRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRT
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llarity 100.0%;
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     biology; cell signalling; insecticide;
                                                                                                                            492
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Pred. No. 3.7e-202;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL0721).

The sequence (ABC0721).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 15111; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000;
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DB; ABL06876.
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                       NAMQVDYIRVY
                                                                 -ALKIDYVRVF
                                                                                                       LFSVDGQVYGEMLNGFTELDENP.
                                                                                                                                                         KLVD----GRSLYGGP-----VLSTDAHQREDLWLSKRKISHFGDDFHTYSLDWSSNRL
                                                                                                                                                                                EFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDW -----
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                                                                                                                                                                                                                                                                                                                      LLFEETFDQLNESLWIHDVRLPLDSKDAEFVLY--DG-KAKVHDGNLVIEP-LLWSSYRP
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                                                   SLGVSVGGFGDF---
                                                                                                                              RFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHF
                                                                                                                                                                                                            TFAFQYGRIEIRAKLPKGDWIVPLLLLEPLTEWYGQSGYESGQLRVALARGNSVLRMPRG
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                                                ·VDHLRTATYEKPWAN--YHPQAKLQFHQAQDQWLPTWKQP---
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Pred. No. 6.8e-25;
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                                                                                                                                                                                                                                                                                                                                                                           133;
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 492;
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                                                                                                                                                                                   -NYGDNFHTFWFDWSPNGL
                                                                                                    RWKQGGPMAPFDKMFYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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                                                                                                                                                                              This sequence comprises the polypeptide precursor of a novel Coerskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase (BG) activity. Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89157). Claimed DNA constructs that encode the novel BG (see Also AAW29455), a mannose binding domain (see AAW29456) or a full-length enzyme, i.e. BG with mannose binding domain (see AAW29456), can be used to produce recombinant BG or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby canabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used to the extracts, pharmaceuticals, food or feed compositions, and to
                                                                                           Query Match
Best Local S
Matches 103
                                                                                                                                                                                                                                                                                                                                                                                            New isolated beta-1,3-glucanase enzyme xanthineolytica, used particularly for for obtaining desirable products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation; fungal cell wall; intracellular product; purification; protoplast
                                                                                                                                         Sequence
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12-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oerskovia xanthineolytica beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW29457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW29457
                                                                                                                                                                                                                                                                                                                                                                                                                                              1997-526451/48.
DB; AAT89157.
   106
                        81
                                              57
                                                                    26
                                                                                                                                                                         protoplasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOVO-NORDISK AS.
                                                                                                       Similarity
                    NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY
                                                         LLWSDEFDGAAGSAPNPAVWNHETGAHGWGNAELQNYTASRANSAL-DGQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xanthineolytica LLG109 (DSM 10297).
                                                                                                                                         303
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                         æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96DK-0000885
96DK-0000427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-DK00160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- Sig_peptide 53..303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                      15.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halkier
                                                                                                                                                                                                                                                                                                                                                                      64pp; English.
                                                                                                                                                                        use in fusion, transformation and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mat_protein
 -GNLVITA-----RREGDGSY---
                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303
                                                                                                     Score 350;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H,
                                                                                         ore 350; DB 18;
ed. No. 1.6e-24;
Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hedegaard

    obtained from Oerskovia
the lysis of microbial cells

                                                                                                              Length 303;
                                                                                           Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protoplast
--TSARMTTQGKY
                                                                                          Gaps
                     140
                                                                   80
                                            105
                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   맑
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RESULT 4
AAW29456
ID AAW2
XX AAW2
XX AAW2
XX AW
AC Oers
XX Beta
XX Beta
XX Oers
XX Oers
XX Oers
YH Key
FT Prot
FT Pont
FT Doma
FT Doma
FT Doma
FT AXX
XX W097
XX W14-4
XX W14-4
XX WPI New
PT New
PT YX New
PT YX New
PT YX YX
XX WPI Dies
XX WPI Dies
XX WPI Dies
XX WPI OR WPI OR WPI
DR WPI OR WPI
DR WPI OR WPI
DR WPI OR WPI
DR WPI
DR
                                                                                                                                                                                                                                  New isolated beta-1,3-glucanase enzyme xanthineolytica, used particularly for for obtaining desirable products
                                                                                                                                                                                                                                                                                                                                                                                                                           Diers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0erskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta-1,3-glucanase; lytic enzyme; yeast;
fungal cell wall; intracellular product;
                                                                                                                                                                                   Example 2; Page 39-40; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9739114-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oerskovia xanthineolytica beta-1,3-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW29456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW29456
                                                                                                                                                                                                                                                                                                                                            1997-526451/48.
DB; AAT89156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 Y 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL
:||:' ::| | :|| | || ||| :| :| :| :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGYPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FHRVTRASVGANAW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPQYGRIEARIQIPRGQGIWPAFWMLGGSFPGTPWPSSGEIDIMENVGFEPHRVHG----
                                                                                                                                                                                                                                                                                                                                                                                                                        Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 xanthineolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96DK-0000885
96DK-0000427
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53..435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TVH-GPGYSGGS-GITGMYQHPQGWSFADTFHTFAVDWKPGEITWFVD--GQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Mannose-binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .435
                                                                                                                                                                                                                                                                                                                                                                                                                           Halkier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLG109
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                                                                                                                                                                                                                                                                                                                                                                                                                           Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DSM
                                                                                                                                                                                                                                                                                                                                                                                                                           Hedegaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10297).
                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                          obtained from Oerskovia
me lysis of microbial cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beta glucan degradation; purification; protoplast
                                                                                                                                                                                                                                                                                                                                                                                                                        ŗ
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                                                                                                                                                                                                                                                                  microbial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protoplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -QQMKVDYVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236
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This sequence comprises the polypeptide precursor of a novel oberskovia xanthineolytica enzyme that exhibits beta-1.3-glucanase (BG) activity and which includes a mannose binding domain (MBD). Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89156). Claimed DNA constructs that encode the novel BG lacking a MBD (see AAW29455 and AAW29457), a MDB (see

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RESULT 5
AAW29455
ID AAW2
XX
AC AAW;
XX
DT 14-;
XX
DE Oer
XX
KW Bet
KW fur
XX
OE
FT CE
FT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 103
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                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                  0erskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                              Oerskovia xanthineolytica mature beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-APR-1998
        23-OCT-1997.
                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                Beta-1,3-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW29455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW29455 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                        WO9739114-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 Y 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGYPDG----TTQLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GF I PDGC INRGGDPALQK PWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDY I RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FHRVTRASVGANAW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPQYGRIEARIQIPRGQGIWPAFWMLGGSFPGTPWPSSGEIDIMENVGFEPHRVHG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NINPOTGAPEGIDEMYNGVLDVWAMYGACINTDNNGCYRTGAAGDIPPAMSARVRTFOKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLWSDEFDGAAGSAPNPAVWNHETGAHGWGNAELQNYTASRANSAL-DGQ------
                                                                                                                                                                                                                                                                                                                  xanthineolytica LLG109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435
                                                                                                                                                                                                                                                                                                                                                                     wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TVH-GPGYSGGS-GITGMYQHPQGWSFADTFHTFAVDWKPGEITWFVD--GQQ
                                                                                                                                 /*tag= }
164..952
                                                                                                                                                                                    23..120
                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                           /*tag=
                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                  e; lytic enzyme; yeast;
intracellular product;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 350; DB
Pred. No. 2.6e
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                product;
                                                                                                                                                                                                                                                                                                               MSG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VFDQPFFLILNVAVGGQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18;
.6e-24;
                                                                                                                                                                                                                                                                                                                                                                purification;
                                                                                                                                                                                                                                                                                                                                                                                           beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96;
                                                                                                                                                                                                                                                                                                                                                                                           glucan degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -QQMKVDYVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW29458) or a full-length enzyme, i.e. BG with mannose binding domain (see AAW29456), can be used to produce recombinant BG polypeptides, with or without a mannose binding domain, in fungation or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, despecially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid sequence was deduced from an isolated genomic DNA sequence (see AAT89155). Claimed DNA constructs that encode the novel BG also AAW29456 for corrected sequence), a mannose binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production of e.g. pigments, colourants, flavourants, yeast extracts, pharmaceuticals, food or feed compositions, and to prepare protoplasts for use in fusion, transformation and compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated beta-1,3-glucanase enzyme xanthineolytica, used particularly for for obtaining desirable products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enzyme that exhibits beta-1,3-glucanase (BG) activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This polypeptide comprises a novel Oerskovia xanthineolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 35-36; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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237 Y
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                                                                                                                                                                                                                                                                                                                              NINPOTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrer
                                                                                                                                                                                                 GIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQA
                                                                                                                                                                                                                                                                    SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL
                                                         PGYPDG
                                                                                  GFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRV
                                                                                                                   FHRVTRASVGANAW
                                                                                                                                                                                                                                       QPQYGRIEARIQIPRGQGIWPAFWMLGGSFPGTPWP-SGEIDIMENVGFEPHRVHG----
                                                                                                                                                                                                                                                                                                                                                             LLWSDEFDGAAGSAPNPAVWNHETGAHGWGNAELQNYTASRANSAL-DGQ------
                                                                                                                                              LLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTN
                                                                                                                                                                              ----TVH-GPGYSGGS-GITGMYQHPQGWSFADTFHTFAVDWKPGEITWFVD--GQQ
237
                            381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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96DK-0000427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Þ,
                                                                                                                                                                                                                                                                                                                                                                                                                                    15.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 340.5; DB 1
Pred. No. 1.1e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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    obtained from Oerskovia
the lysis of microbial cells

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transformation and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                       95;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 133;
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                                                                                                                   ·VFDQPFFLILNVAVGGQW
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                                                         -QQMKVDYVRV
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Best Local S
Matches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of a mature lipopolysaccharide (LPS) binding protein from Bombyx mori. The protein was isolated from the haemolymph of fifth stage B.mori larvae after injection with Enterobacter cloacae strain 57-9. Partial amino acid sequence was used to generate PCR primers (AAT10280-1). These amplified a fragment of the gene used as a probe to obtain the full length gene (AAT10879) by screening a cDNA library derived from B.mori previously injected with heat-killed E.cloacae. The protein or fragments of it, can be used to treat diseases associated with LPS complexes e.g. septic shock, to remove LPS from products used for injection and to protect transgenic plants e.g. vines, tobacco, tomato or potato, against fungal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New protein from Bombyx mori that binds bacterial lipopoly-saccharide - esp. used to treat septic shock, also encoding it, for producing transgenic plant(s) resistant to feet the second secon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUN-1994;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FR2721032-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lipopolysaccharide binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                            188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lysaccharide binding protein; Bombyx mori; haemolymph; primer; bacter cloacae; PCR; polymerase chain reaction; amplification; LPS-complex; septic shock; injection; transgenic plant; vine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INST PASTEUR
GGEFLGIQKMGSTMHWGPGWD-DNRYWLISLPKHSDDWNYGDNFHTFWFDWSPNGLRFFV : | ::||:||: | ::|: ; |
                                                                                                            HGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWP-RSGEIDIIETIGN-----RDFKNT
                                                                                                                                                                                                                            TGAP-FGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI-PPAMSARVRTFQKYSFT
                                                                          YGTVEIRAKLPQGDWLYPEILLEPFLKKYGSMNYASGVVKIACARGNAELYSGPNDYSNT
                                                                                                                                                                                 QHMPGFLDDSIYSGTLN---LFSGCTSS-AEACIKQASGADILPPIVSGRI-TSIGFAFT
                                                                                                                                                                                                                                                                                 IFEEQFDSLDENVWQIEQYIPIYHPEYPFVSYQRNNLTVSTADGNLHI:-----NAKLQ
                                                                                                                                                                                                                                                                                                                                 VWQDEFDYFDGAKWQ-HEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tomato; potato; fungal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 170
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27.3%;
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                                                                                                                                                                                                                                                                                                                                                                                              58;
                                                                                                                                                                                                                                                                                                                                                                                         Score 314; DB
Pred. No. 6.8e
58; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
.8e-21;
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                                                                                                                                                                                                                                                                                                                                                                                           143;
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                                                                                                                                                                                                                                                                                                                                                                                         68;
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RESULT 7
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                                                                                                                 Claim 5;
                                                                                                                                    attack
                                                                                                                                          New protein from Bombyx mori that binds bacterial lipopoly-saccharide - esp. used to treat septic shock, also DNA encoding it, for producing transgenic plant(s) resistant to fung
                                                                                                                                           lipopoly-saccharide encoding it, for pro
                                                                                                                                                                                            WPI; 1996-060094/07
                                                                                                                                                                                                              Brey PT,
                                                                                                                                                                                                                                                     09-JUN-1994;
                                                                                                                                                                                                                                                                       09-JUN-1994;
                                                                                                                                                                                                                                                                                                            FR2721032-A1
                                                                                                                                                                                                                                                                                                                                                                              Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacter cloacae; PCR; polymerase chain reaction; ampl
probe; LPS-complex; septic shock; injection; transgenic pl
tobacco; tomato; potato; fungal infection; fungus.
                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bombyx mori full length LPS-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR89137
                                                                                                                                                                                                                                                                                           15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                           Bombyx mori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR89137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       lipopolysaccharide binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303
                                                                                                                                                                                   AAT10279
                                                                                                               Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                               Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SLIVDFVKV 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAMOVDYIRV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK----FFDARGNWKWTWDDEGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGGITEF-RDGSITSGG---VTKPW-----RDSARKASVHFWRHMSDWFPRWSQP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGEEWARVEAPRDAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----VLYGGPIMDLECRENFLSTKRRRDGTSWGDSFHTYSVQWTPDFIALSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                42-43;
                                                                                                                                                                                                                                                                       94FR-0007083.
                                                                                                                                                                                                                                                                                                                                          /note=
182
                                                                                                                                                                                                                                                                                                                                                            /note=
13..467
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                             53pp;
                                                                                                                                                                                                                                                                                                                              "putative N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                     "signal
                                                                                                                                                                                                                                                                                                                                                  "mature protein"
                                                                                                                French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     467
                                                                                                                                                                                                                                                                                                                                                                     peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bombyx mori; haemolymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAVCAHAPRHLLQAGSQMAPFDDHFYITLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                     ph; primer;
lification;
lant; vine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443
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This is the amino acid sequence of the full length lipopolysaccharide (LPS) binding protein from Bombyx mori. The protein was isolated from the haemolymph of fifth stage B.mori larvae after injection with Enterobacter cloacae strain 57-9. Partial amino acid sequence was used to generate PCR primers (AAT10280-1). These amplified a fragment of the gene used as a probe to obtain the full length gene by screening a CDNA library derived from B.mori previously injected with heat-killed E.cloacae. The protein or fragments of it, can be used to treat diseases associated with LPS complexes e.g. septic shock, to remove LPS from protein or fragments of the protein or protein the first threat the protein or the second for the protein or fragments of it.

products used for injection and to protect transgenic plants tobacco, tomato or potato, against fungal infections.

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RESULT 8
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Best Local Sim
Matches 101;
The new enzyme is derived from alkaoplhilic Bacillus Sp. The enzyme acts on beta-1,3-glucans to form glucose and laminaribiose. It is stable over a wide pH range with opt. activity at weakly actidic pH and has good heat resistance.
                                        Claim 7; Fig 2; llpp; Japanese
                                                      Heat resistant beta-1,3-glucanase alkali-compatible Bacillus sp.
                                                                               WPI; 1991-113290/16.
N-PSDB; AAQ11293.
                                                                                                                       20-JUL-1989;
                                                                                                                                     20-JUL-1989;
                                                                                                                                                     07-MAR-1991
                                                                                                                                                                     JE03053883-A.
                                                                                                                                                                                    Bacillus sp
                                                                                                                                                                                                    Alkalophilic;
                                                                                                                                                                                                                    Beta-1,3-glucanase
                                                                                                                                                                                                                                    25-MAR-2003
18-JUN-1991
                                                                                                                                                                                                                                                             AAR11599;
                                                                                                                                                                                                                                                                           AAR11599 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                      (SHKJ ) SHINGIJUTSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QHMPGFLDDSIYSGTLN---LFSGCTSS-AEACIKQASGADILPPIVSGRI-TSIGFAFT
                                                                                                                                                                                                                                                                                                                   -SLIVDFVKV 464
                                                                                                                                                                                                                                                                                                                                                 AAGGITEF-RDGSITSGG---VTKPW-----RDSARKASVHFWRHMSDWFPRWSQP---
                                                                                                                                                                                                                                                                                                                                                                                 DGEEWARVEAPRDAL:
                                                                                                                                                                                                                                                                                                                                                                                                                               GGEFLGIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFV
                                                                                                                                                                                                                                                                                                                                                                                                                                              YGTVEIRAKLPQGDWLYPEILLEPFLKKYGSMNYASGVVKIACARGNAELYSGPNDYSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAP-FGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI-PPAMSARVRTFQKYSFT
                                                                                                                                                                                                                                                                                                                                  NAMOVDYIRV
                                                                                                                                                                                                                                                                                                                                                                AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK----FFDARGNWKWTWDDEGDN
                                                                                                                                                                                                                                                                                                                                                                                                               -----VLYGGPIMDLECRENFLSTKRRRDGTSWGDSFHTYSVQWTPDFIALSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFEEQFDSLDENVWQIEQYIPIYHPEYPFVSYQRNNLTVSTADGNLHI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467
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(first entry)
                                                                                                                                                                                                     heat resistant.
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                                                                                                                       89JP-0185928
                                                                                                                                      89JP-0185928
                                                                                                                                                                                                                                                                            Protein;
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                                                                                                       KAIHATSU
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                                                               gene
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                                                               DNA
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AAB99272
ID AAB9
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AC AAB9
XX
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밁
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Query Match
The present sequence is beta-1,3-glucanase from I protein can be used in various industrial fields cake and bread manufacture and brewing.
                                                                                                      Beta-1,3-glucanase and beta-1,3-glucan-binding
                                                                                                                                  WPI; 2001-364762/38.
N-PSDB; AAH46359, AAH46360.
                                                                                                                                                                                                             01-NOV-1999;
                                                                                                                                                                                                                                                                     08-MAY-2001.
                                                                                                                                                                                                                                                                                                   JP2001120280-A.
                                                                                                                                                                                                                                                                                                                                Bacillus circulans
                                                                                                                                                                                                                                                                                                                                                              beta-1,3-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                           Bacillus circulans
                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB99272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB99272 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                         Claim 1; Page 8-9; 12pp; Japanese
                                                                                                                                                                                                                                         01-NOV-1999;
                                                                                                                                                                              (MEIJ ) MEIJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 YSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEF 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --MLVDYVRVYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGT-NLAPFDQNFHF 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGIQKMGSTWHWGPGWDDNRYWLTSLPKHSDDWNYG------DNFHTFWFDWSPNGLR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WSLVWSDEFNGNSLNPANWTAEIGTGSGGWGNNELQYYTSRPQNLQVSGGNLII--TAQR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GTVH----WDAN-----GHAE---YGRTSGNLDFSQYHTYSVEWEPNYIR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSFRYGKIEARIKLPSGQGLWPAFWMLGEDFSSVGWPYCGEIDIMERVNNNPHVN----- 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILNLAVGG-----
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                                                                                                                                                                            SEIKA KAISHA LTD
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                                                                                                                                                                                                                                                                                                                                                                                           beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                            enzyme; stockbreeding; bread
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234
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Pred. No. 7.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
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                                                                                                      peptide
               Bacillus
Is such as
                                                                                                                                                                                                                                                                                                                                                               manufacture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 261;
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                                                                                                        and
               circulans. The stockbreeding,
                                                                                                        their genes
                                                                                                                                                                                                                                                                                                                                                              brewing.
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                             The
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                        Beta-1,3-glucanase; Cellulomonas cellulans; Bacillus subtilis; lytic enzyme; beta-glucan degradation; cell wall lysis; pigment; colorant; flavour; yeast extract; protoplast.
                                                                                                                                                                                                                                                                                 Oerskovia beta-1,3-glucanase.
WPI; 1996-222000/22.
                   Savva
                           Asenjo JA,
                                                                 14-OCT-1994;
                                                                                                        25-APR-1996
                                                                                                                          WO9612013-A1
                                                                                                                                                       Protein
                                                                                                                                                                         Peptide
                                                                                                                                                                                                                           Oerskovia
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                                                                                                                                                                                                                                                                                                                          AAR97362;
                                                                                                                                                                                                                                                                                                                                           AAR97362 standard;
                                                                                    16-OCT-1995;
                                                                                                                                                                                             Peptide
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                                              (NOVO ) NOVO-NORDISK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDN----FHTFWFDWSPNGLRFFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WNLVWSDEFNGTSLNRANWTPEIGTGSGGWGNNELQYYTDRAQNVQVTGGNLVI--TAQK 61
                                                                                                                                                                                                                                                                                                                                                                                                             VDYIRVYK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                   AVGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQ 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GTVHWDAG------GHADFGRVSGNLDFSQFHVYSIEWDSKYIRWFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSFTYGKVEARIKLPSGQGLWPAFWMLGSNISSVGWPKSGEIDIMERVNNNPYVN-----
                                                                                                                                                                                                                         xanthineolytica strain LLG109 (DSM 10297).
                           Diers I,
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                                                                                    95WO-DK00414
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                                                                                                                                             /label= Pro_peptide 64..306 /label= Mat_protein
                                                                                                                                                                          /label= Sig_peptide 36..63
                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           234
                                                                                                                                                                                                                                                                                                                                           Protein;
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                           Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                  NWPGSPNNSTPFP
                                                                                                                                            Mat_protein
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                                                                                                                                                                                                                                                                                                                                            306
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Pred. No. 3.1e-20;
17; Mismatches 90;
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                            Halkier
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                          Hedegaard
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RESULT 11
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Best Local S
Matches 93
                                                                                                          Drosophila melanogaster
                                                                                                                                                                pharmaceutical
                                                                                                                                                                                          Drosophila;
                                                                                                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A novel beta-1,3-glucanase (AAR97362) from Oerskovia xanthineolytica LLG109 is useful for degrading or modifying beta-glucan-contg. material. Its amino acid sequence was deduced from a genomic DNA sequence (AAT29043) isolated from an O. xanthineolytica library. Recombinant beta-1,3-glucanase can be produced on a large scale using transformed host cells, esp. Bacillus subtilis DN1885 or ToC46. Protease-free beta-1,3-glucanase can be obtd. that is useful for lysing fungal cell walls, allowing recovery of intracellular proteins. The enzyme is also useful for the prepn. of protoplasts and for the prodn. of pigments, colorants, flavours, yeast extract
                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                              ABB61180
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                                                                                                                                                                                                                                                                                                                                                                                                                  standard; Protein;
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                                                                                                                                                                                          developmental biology; cell signalling; insecticide;
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27-SEP-2001 WO200171042-A2

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
 18-AUG-1998
                    AAW56275;
                                       AAW56275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 10332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE
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                                       standard;
                                                                                                                                   WAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFF
                                                                                                                                                                                                                                                                                                                LVFVDEFNAAKLDPNKWKAERRFSGQPDYEFNVYVDDAPETLCLANGHVVLSTNTMKKQF
                                                                                    KEVKKIRDHWLDEGH--
                                                                                                     DARGNWKWTWDDEGDNNAMQVDYIRVY 381
                                                                                                                        LEEGTGLAPFDQEFYLTFGLSVGGFNEYQHE
                                                                                                                                                                                VDDENQALLDVPYPLIDANPWWVDFWEWGKPW-----
                                                                                                                                                                                                   AVLFADEPLRSVKNCLKPGTG
                                                                                                                                                                                                                    GGEFLG--IQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFF
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                                                                                                                                                                                                                                                         YSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYG-GWPRSGEIDIIETI---GNRDFKNT
                                                                                                                                                                                                                                                                                                                                  IVWQDEFD--YFDGAKWQHEVTATGGGNSEFQLYTQDGANSF-VRDGKLFIKPTLLADNI
                                                                                                                                                                                                                                                                                            NPQTGAPFGTDFMYNGVLDVWAMYGACTNTDN-NGCYRTGAA--GDIPPAMSARVRTFQK
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                                                                                                                                                                                                                                                                                                                                                   Score 295; DB
Pred. No. 4.6e
7; Mismatches
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No. 4.6e-19;
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                                                                                                                                                              -GKEWCVQGSAKGSFSETTAAGKSLPQAQK---
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Best Local (
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N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                        173
                                                                                             113
 302
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The present sequence represents the Flavobacterium keratolyticus endo-beta-galactosidase (designated ENDO-A) protein. The ENDO-A protein can be used in conjugation with alpha-N-acetylgalactosaminidase to remove externally and internally linked A antigen on group Al erythrocytes. The resulting erythrocytes may be transfused into individuals who would be otherwise unable to safely tolerate a transfusion of type Al blood. The ENDO-A protein can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated endo-beta-galactosidase - from Flavobacterium keratolyticus, used particularly for de-antigenising human erythrocytes bearing Al antigen for blood transfusions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-N-acetylgalactosaminidase;
erythrocyte; transfusion; blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               degrade keratan sulphate (e.g. in the food industry),
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DB; AAV22722.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig
APFDQNFHFILNVAVG-GTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW
                                            TMIWSPNDIRFYV --- NNSL--
                                                                                    WFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNL
                                                                                                                                                                         DITETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTF
                                                                                                                                                                                                                                         AGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPED-WVYGGWPRSGEI
                                                                                                                                                                                                                                                                                                        NLVLR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                LLFGEGFAFTDWDQYHIVWQDEFDY---FDGAKWQHEVTATGGGN---SEFQLY-TQDGA
                                                                                                                                 DSMEHVNNESV--
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47..422
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Pred. No. 2.4e-18;
2; Mismatches 100;
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typing reaction; keratan
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                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences (ABL0184)
(ABB57737-ABB72072)
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11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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genes from Drosophila and
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pharmaceutical.
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DB; ABL04547.
136 TFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFK-N 194
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                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                 DNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI----PPAMSARVR 135
                                                                                                                                                                                    QGELIFEDNFSEAQLNKTTWKHDIRQRMYHVEEELVAFDDAARNCFVKEGELHIVPTIAT 170
                                                                                                                                                                                                                                     QYHIVWQDEFD--YFDGAKWQHEVTATGGGNSEFQLYTQDGA-NSFVRDGKLFIKPTLLA
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                                                                                                                                                                                                                                                                                                                                                                                                   410 AA;
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2000US-0614150.
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24.5%;
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Pred. No. 6.9e-15;
2; Mismatches 143
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RESULT 14
ABB60451
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Query Match
Best Local Similarity 24.9
Matches 91; Conservative
                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIJ6176-ABIJ63511), expressed DNA sequences (ABIJ6176-ABIJ63511), expressed DNA sequences (ABIJ6176-ABIJ63511).
                                                                      The sequence data for this patent did not form specification, but was obtained in electronic f at ftp.wipo.int/pub/published_pct_sequences.
                                                  Sequence
                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB60451 standard;
                                                                                                                                                                                                                        Disclosure; SEQ ID
                                                                                                                                                                                                                                                                        New isolated nucleic
                                                                                                                                                                                                                                                                                                              WPI:
                                                                                                                                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB60451;
                                                                                                              (ABB57737-ABB72072)
                                                                                                                                                                                                                                                 interactions
                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
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DB; ABL04554.
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2000US-0614150
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            11.1%;
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                                                                                                                                                                                                                                                                                                                                    PWD,
                                                                                                                                                                                                                                                          detection reagent for detecting for elucidating cell signalling
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Score 249.5; DB Pred. No. 6.9e-12; Mismatches 1
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Peptide
AAQ81334 encodes AAR67915 a (1-3)-beta-D-glucan sensitive factor, it has a high affinity for the (1-3)-beta-D-glucan found in fungal
                                   Claim 9; Pages 23-32; 51pp; Japanese.
                                                                   DNA encoding a polypeptide comprising a tetrapeptide motif at least once - which may be used as an antibacterial and
                                                                                                       WPI; 1995-060996/08.
N-PSDB; AAQ81334.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR67915;
                                                                                                                                                                                     29-JUN-1993;
                                                                                                                                                                                                           29-JUN-1994;
                                                                                                                                                                                                                                  12-JAN-1995.
                                                                                                                                                                                                                                                       WO9501432-A1
                                                                                                                                                                                                                                                                                                                          Limulus sp.
                                                                                                                                                                                                                                                                                                                                                mycosis diagnosis.
                                                                                                                                                                                                                                                                                                                                                       (1-3)-beta-D-glucan sensitive factor; antifungal agent;
                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR67915 standard; Protein;
                                                                                                                                        Iwanaga S,
                                                                                                                                                              (SEGK ) SEIKAGAKU KOGYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                (1-3)-beta-D-glucan sensitive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGELIFEDNFSEAQLNKTTWKHDIRQRMYHVEEELVAFDDAARNCFVKEGELHIVPTIAT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAMVIDYVRVY 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRNSFSFKFGKIVVRAKLPKGDWLFPYLMLQPVS-TYAETHYAKQLRIAYARGNANLRTK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E-----VTDGSFK-----LGDRCTAVESPEQECNIAHGIFYSIKPPVFSAQIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI----PPAMSARVR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QYHIVWQDEFD--YFDGAKWQHEVTATGGGNSEFQLYTQDGA-NSFVRDGKLFIKPTLLA
                                                                                                                                        Muta T,
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(first entry)
                                                                                                                                                                                     93JP-0184403
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1..19
/label= sig_peptide
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Best Local S
Matches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell walls. The protein is therefore useful for clinically diagnosing mycosis, and as an antifungal agent for the removal of fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Updated on 25-MAR-2003 to correct PN field.)
240
                353 FFDARGNWKWTWDDEGDNNAMQVDYIRVYK 382
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                                                                                                                                                                                                                                                      119 RTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRS 178
                                                                                                                                         234 -YGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYEND
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                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                       KIQGGVNGKSAFRNKVFVILNMAIGGN-----
                                                                                                                                                                                         GEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLP----KHSDDWN 233
                                                                                                                                                                                                                             YT-----SARLKTQFDKSWKYGKIEAKMAIPSFRGVWVMFWMSGDNTNYVRWPSS
                                                                                                                                                                                                                                                                                                        QDGANSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCY 118
:: |: | | | | | | |
                                                                                                               TNGIDYHIYSVEWNSSIVKWFVNGN-------
                                                                                                                                                                       GEIDFIE-----HRNTNNE----KVRGTIHW---
                                                                                                                                                                                                                                                                                      LVLLCCVVLHVGVARICCSHEPKWQLVWSDEFTNGISSDWEFEMGNGLNGWGNNELQYYR 61
                                                                               NPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK 352
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Pred. No. 8.5e-11;
9; Mismatches 106
-MYIDYVRVYQ
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Search completed: September 16, 2003, 11:25:56 Job time: 120.038 secs

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1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
4: /cgn2_6/ptodata/1
5: /cgn2_6/ptodata/1
6: /cgn2_6/ptodata/1
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Match
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-330-945-37
US-09-159-106-13
US-09-159-106-13
US-09-159-106-13
US-09-159-106-2
US-08-12-072C-2
US-08-712-072C-2
US-08-712-072C-2
US-08-712-072C-2
US-08-712-072C-2
US-08-712-072C-2
US-08-713-0745-2
US-08-713-056-4
US-09-266-690-10
US-09-266-690-10
US-09-266-690-731-8
US-09-268-772-2
US-08-714-741-41
US-09-719-402A-2
US-08-713-998-2
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13, Appl
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14, Appl
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US-08-712-072C-3
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US-08-712-072C-3
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Query Match
                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 OI
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                        STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: P
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, Elizabeth A
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIDM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: >\CITY: New York
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CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/712,072C FILING DATE: 11-SEP-1996
                                                                                                                                                                                                                                                                                                                                  LENGTH:
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US-09-1486-072-1

US-09-194-612A-1

US-09-719-402A-6

US-09-604-957-3

US-09-360-237-1

US-09-360-237-27150

US-09-252-991A-27150

US-09-216-295-21

US-09-216-295-21

US-09-216-295-21

US-09-319-861A-1

US-09-739-861A-1

US-09-739-861A-5

US-09-739-861A-5

US-09-739-861A-5

US-09-739-861A-5

US-09-795-583-5

US-09-795-583-5

US-09-795-583-5

US-09-286-609A-4
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Length 321;

Minimum Maximum

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Total number Searched:

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RESULT 2
US-08-392-828C-37
; Sequence 37, Application US/08392828C
; Patent No. 5795962
; Patent No. 5795962
                                          ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-(
TELECOMMUNICATION INFORMATION:
TELECHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: IWANAG
                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL POTITIES OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
                                                                                                                                                                                              APPLICATION NUMBER: US/0:
FILING DATE: 28-FEB-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
STRANDEDNESS:
                              LENGTH:
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                               262 amino acids
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SEKI, NORIAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IWANAGA, SADAAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                             THIBEAULT
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US-09-330-945-37
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Best Local S
Matches 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Applic Patent No. 6077946
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/330,945
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                          CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
TITLE OF INVENTION: AMEBOCYTE LYSATE FACTOR G SI
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: IWANAGA, SADAAI
APPLICANT: MUTA, TATSUSHI
APPLICANT: SEKI, NORIAKI
APPLICANT: ODA, TOSHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 100; Conserv
                                                                                                                                                                                                  COUNTRY: UZIP: 02110
                                                                                                                                                                                                                                                   CITY: BOSTON
                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /note- "BG1 A1 SEQUENCE (FIGURE 2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIVWQDEFD--YFDGAKWQHEV-----TATGGGNSEFQLYTQDGANSFVRDGKLFIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KWTWDDEGDNNAMQVDYIRVYK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFDQNFHFILNVAVGGT--NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIKWYVDGKFFYKVTNQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLRFFVDDE-----NQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG-----SSGGDYHFPEGQTFANDYHVYSVVWEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGEELGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWN-----YGDNEHTFWFDWSPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A-----NNDSKSFPQDP----NRYAQYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TMQVDYVRVYK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFDEPFYLIMNLAVGGNFDGGRTP----NASDIPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTKDKLSLKYGRVDFRAKLPTGDGVWPALWMLPKDSVYGTWAASGEIDVMEARGRLPGSV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09330945
                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                         IWANAGA, SADAAKI
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                                                                                                                                                                                                                                                                                   PATENT ADMINISTRATOR, THIBEAULT, LLP
                                                                                                                                                                                                                                                                   HIGH
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26.2%;
            09/119,995
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Pred. No. 3.2e-27;
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                                                                                                             Version
                                                                                                                                                                                                                                                                                                     TESTA, HURWITZ
                                                                                                               #1.25
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GENERAL INFORMATION:

APPLICANT: Perrer, Pau
APPLICANT: Halkier, Torben
APPLICANT: Halkier, Torben
APPLICANT: Hedegaard, Lisbeth
TITLE OF INVENTION: An Enzyme With -1,3-Gluc
TITLE OF INVENTION: Activity
FILE REFERENCE: 4693,204-US
CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER APPLICATION NUMBER: 0885/96
EARLIER APPLICATION NUMBER: 0885/96
EARLIER APPLICATION NUMBER: 9885/96
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1996-08-23
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: LOCATION: 1..262
: OTHER INFORMATION: /note- "BG1 A1 SEQUENCE (FIGURE US-09-330-945-37
                                                                                                                                                                                                                                                                                                                  Sequence 13, Application Patent No. 6284509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.7%;
Best Local Similarity 26.2%;
Matches 100; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 27, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 NLIWQDEFNGTTLDTSKWNYETGYYLNNDPATWGWGNAELQHYTNSTQNVYVQDGKLNIK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLRFFVDDE-----NQALLDVPYPLIDANFWWVDFWEWGKPWLPQYENDNPWAGGTNLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWN-----YGDNFHTFWFDWSPN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTKDKLSLKYGRVDFRAKLPTGDGVWPALWMLPKDSVYGTWAASGEIDVMEARGRLPGSV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SG-----TIHFGGQWPVNQ-----SSGGDYHFPEGQTFANDYHVYSVVWEED 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTILLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFDEPFYLIMNLAVGGNFDGGRTP----NASDIPA--
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                                                                                                                                                                                          -1,3-Glucanase
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; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11
                                                                                                                                                                                                                                     APPLICANT: Hedegaard, Lisbeth
TITLE OF INVENTION: An Enzyme With -1,3-Gluc
TITLE OF INVENTION: An Enzyme With -1,3-Gluc
TITLE OF INVENTION: Activity
FILE REFERENCE: 4693.204-US
CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER APPLICATION NUMBER: 085/96
EARLIER FILING DATE: 1996-12-04
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: 085/96
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER APPLICATION NUMBER: PCT/DK97/00160
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US-09-159-106-11
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; TYPE: PRT
; ORGANISM: Oerskovia
US-09-159-106-13
  Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 13
LENGTH: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Appli
Patent No. 6284509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                         EARLIER FILING DATE: 1997-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Halkier, Torben
                                                                                                                                            LENGTH: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
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15.6%; Score 350; DB 3; Length 435; 28.5%; Pred. No. 9.4e-27; ive 30; Mismatches 96; Indels 1
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Conservative

Indels 132;

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RESULT 6
US-08-712-072C-4
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                                                                                                        TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                NAME: BOGOSÍAN, Elizabeth A.
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 634
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
           MOLECULE TYPE:
                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/712,072C FILING DATE: 11-SEP-1996
                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                       TOPOLOGY:
                                                  STRANDEDNESS:
                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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(212) 286-0854 or 286-0082
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US-09-159-106-2
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ORIGINAL SOURCE:
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; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-2
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                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: An Enzyme With .-1,3-Glucanase TITLE OF INVENTION: Activity FILE REFERENCE: 4693.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ferrer, Pau
APPLICANT: Diers, Ivan
APPLICANT: Halkier, Torben
APPLICANT: Hedegaard, Lisbeth
                                                                                                                                                                                                                                                                                                            EARLIER FILING DATE: 1997-04-14
                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: PCT/DK97/00160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 WVYGG--WPRSGEIDIIETIG-NRD-----FKNTGGEFLGIQKMGSTMHWGPGWDDNRY 220
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                 1 MRWTLVVLCLLFGEGFAFTD-----WDQYHIVWQDEFDYF---DGAKWQHEVTATGGG 50
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LLWSDEFDGAAGSAPNPAVWNHETGAHGWGNAELQNYTASRANSAL-DGQ--
                                                                                                                                                                                                                                                                           for Windows Version 3.0
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                                                                            Score 340.5; DB 3;
Pred. No. 4.1e-26;
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Query Match 13.7%; Score 307; DB 2; Length 306; Best Local Similarity 26.2%; Pred. No. 1.2e-22; Matches 95; Conservative 36; Mismatches 97; Indels 134; Gaps	; INFORMATION FOR SEC ID NO: 2: ; SEQUENCE CHARACTERISTICS; ; LENGTH: 306 amino acids ; TYPE: amino acids ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-824-707-2	23733	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION UMBEER: US/08/824,707 FILING DATE: 14-April-1997 CLASSIFICATION: 435 CLASSIFICATION: 435 CLASSIFICATION: 436	STATE: New YOLK STATE: New YOLK COUNTRY: U.S.A. ZIP: 10174-6401 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: TRM DC COMPANIAN	CORRESPONDENCE ADDRESS: ADDRESSEE: No. 59196880 No. 5919688disk of No. 5919688th America, Inc. STREET: 405 Lexington Avenue, Suite 6400	; APPLICANT: Asenjo, Juan ; APPLICANT: Savva, Demitris ; TITLE OF INVENTION: No. 5919688el enzyme with beta-1,3-glucanase activity ; NUMBER OF SEQUENCES: 4	Ferrer, Diers, Hedegaam	RESULT 8 US-08-824-707-2 ; Sequence 2, Application US/08824707 ; Patent No. 5919688	Db 237 ¥ 237	Qy 381 Y 381	Qy 321 GFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRV :	Qy 261 LLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPEDQNFHFILNVAVGGTN :	Qy 201 GIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQA:	Qy 141 SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL:	Qy 81 NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 14
; STKANDEDNESS: ; TOPOLOGY: Inear ; MOLECULE TYPE: peptide ; HYPOTHETICAL: NO	TELEPHONE: (212) 697-5995 TELEFAX: (212) 286-0854 or 286-0082 TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 285 antino acids TYPE: amino acid	; FILING DATE: ; FILING DATE: ; ATTORNEY/AGENT INFORMATION: ; NAME: BOGOSIAN, E11zabeth A. ; REGISTRATION NUMBER: 39,911 ; REFERENCE/DOCKET NUMBER: 39,917 ; REFERENCE/DOCKET NUMBER: 64475/97 ; TELECOMMUNICATION INFORMATION:	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/712,072C FILING DATE: 11-SEP-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA:	PUT	ADDRESSEE: ASTREET: 90 F	; APPLIC ; TITLE ; NUMBER	RESULT 9 US-08-712-072C-5 ; Sequence 5, Application US/08712072C ; Patent No. 5925541 ; GENERAL INFORMATION:	Db 300 VY 301	278	Qy 320 NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQYDYIR 379	380 Qy 260 ALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGT 319 36	320 QY 201 GIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFYDDENQ 259	260 Qy 141 SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL 200	200 QY 81 NINPQTGAPEGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140	26 IVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLAD 80 :

Length Indels 155; 422;

Gaps

-AGD- 108

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RESULT 10
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Best Local Similarity
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                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb
COMPUTER: IBM PC COMPATIBLE
         ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, Elizabeth A.
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                   SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE NUMBER OF SEQUENCES: 13
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ORIGINAL SOURCE:
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SOFTWARE: ASCII
                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 11-SE
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STREET: 9
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 TELEFAX:
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286-0854 or 286-0082
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Pred. No. 1.2e-20;
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US-08-392-828C-2
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Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                  Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
            ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR,
ADDRESSEE: THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE NO
                                                                                                                                                                                                                  TITLE OF INVENTION:
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ORIGINAL SOURCE:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                               APPLICANT:
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                 COUNTRY:
                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                       , Application 5795962
                                                                                                                              BOSTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPAMSARVRTFQKVSFTHGRVVVHAK-----MPV---GDWLWPAIWMLPED-WVYGGWPR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNLYTMIWSPNDIRFYV---NNSL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLNATTVATTD---YELIWSDEFNSSGGFDSTKWSYADRGTVAWNK--YMTSQDGSNLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTNLAPFDQNFHFILNVAVG-GTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAG
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                                                                                                                 MA
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SEKI, NORIAKI
ODA, TOSHIO
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27.2%;
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             Release #1.0,
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Pred. No. 5.3e-19;
Pred. No. 5.3e-19;
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               Version
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                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 248-710
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                         APPLICANT: ODA, TOSHIO
TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
TITLE OF INVENTION: AMEBOCYTE LYSATE FACTOR G SUBUNIT
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJJ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                  PPLICANT:
                                                                                                                                                                                                                                                                   PPLICANT:
                                                                                                                                                                                                                                                                                     PPLICANT:
                                                        STATE: MA
COUNTRY: USA
                                                                                          CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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Similarity 21.5%;
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MUTA, TATSUSHI
SEKI, NORIAKI
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                                                                                                         HIGH STREET
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17) 248-7100
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Pred. No. 2.9e-12;
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RESULT 13
US-08-737-526-4
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                                                                                                                                           Sequence 4, Application
Patent No. 5871966
GENERAL INFORMATION:
APPLICANT: Kofod, I
APPLICANT: Andersen
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Matches
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TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
               CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58719660 No.
                                                    APPLICANT: Kauppinen, Markus Sakari
APPLICANT: Christgau, Stephan
TITLE OF INVENTION: An Enzyme With Endo-1,3(4)-B-Glucanase
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 6
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REFERENCE/DOCKET NUMBER: FJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
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227 IDYVRVYQ 234
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                                                                                                                                                                                                                    Application US/08737526
405 Lexington Avenue
                                                                                                                                           Kofod, Lene Venke
Andersen, Lene No.
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                    5871966disk of No.
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                  5871966th America,
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US-09-098-580-4
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Best Local S
Matches 85
                          GENERAL INFORMATION:
APPLICANT: Kofod, I
APPLICANT: Kandersei
APPLICANT: Kauppin
APPLICANT: Christy
                                                                                                   Sequence 4, Application US/09098580 Patent No. 6140096
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REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION IMPORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOSS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,526
FILING DATE: 08.NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 292 amino
TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                    ARGNWKWTWDDEGDNNAMQVDYIRVY
                                                                                                                                                                                                                                                                                                             ---QSETLTWSLDGTIYFQITGS----
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                                                                                                                                                                                                                                                   ---NNIA--HSPLFFILNVAVGG-----
                        Andersen, Lene No. 61400
Kauppinen, Markus Sakari
Christgau, Stephan
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                                                                       Rofod, Lene Venke
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An Enzyme With Endo-1,3(4)-B-Glucanase Activity
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RESULT 15
US-07-985-458-3
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/737,52
FILING DATE: 08-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Valeta, Gregg A
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61400960 No. 6140096disk of
STREET: 405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: Z12 U.
TELEPHONE: Z12-878-9655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                               166 V---DGQATGHGTLHCDVYPGGICNEGNGI-GGPVNIANVNDWHAWRVEIDRTPSSW---
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85; Conserv
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                                                                                          ARGNWKWTWDDEGDNNAMQVDYIRVY
                                                                                                                                          AGGTNLAPEDQNEHFILNVAVGGTNGEIPDGCINRGGDPALQKPWSNGDWYNDAMRKEFD
                                                                                                                                                                                                               DNFHTEWEDWSPNGLREEVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPW 295
                                                                                                                                                                                                                                                             IGNRDEKNTGGEEL-----GIQKMGSTMHWGP----GWDDNRYWLTSLPKHSDDWNYG 235
                                                                                                                                                                                                                                                                                                        KYTFTPAAGKVTRLEAAIRFGSNAQANKQGIWPAFWMLGDSLRQPGGSWPNCGEIDIMET
                                                                                                                                                                                                                                                                                                                          KYSFT--HGRVV-VHAKMPVG------DWLWPAIWMLPEDWVY--GGWPRSGEIDIIET 186
                                                                                                                                                                                                                                                                                                                                                                      --QLVPWRDSSKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                 FNLVWTDTFAGNGGTSPNQNNW-NIITGNLNVNAEQETYSSSTANVQLSGGS----TL-
                                                                                                                                                                                   ---QSETLTWSLDGTIYFQITGS----
                                                                                                                                                                                                                                                                                                                                                                                               ADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQ 138
                                                                                                                        ---NNIA--HSPLFFILNVAVGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 amino acids
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22.0%; Pred. No. 7e-
ative 40; Mismatches
                                                             DGYGSMMEVGYVAQY
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7e-05;
110;
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                                                                                                                                                                                    RIGNOGVW
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Sequence 3, Application US/07985458 Patent No. 5344777

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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/985,458
FILING DATE: 19921203
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/658,221
FILING DATE: 20-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS D
SOFTWARE: ASCII FORM
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10016-2088
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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ADDRESSEE: Frishauf, Holtz,
                                                                                                                                                                                                                                                   STRAIN: MH-24
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)972-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-MAR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (**
TELEFAX: 236268
                                                                                                                                                                                                                                                          RIGINAL ACCORDANISM: ACCORDANISM: MH-24
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                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD: IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MATURE PEPTIDE LOCATION: 36 to 738
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 738 amino acids TYPE: amino acid TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
                  polyoxogenes
                               Beppu, Teruhiko
Cloning and Sequencing of the Gene Cluster
Encoding Two Subunits of Membrane-Bound
Alcohol Dehydrogenase from Acetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600 Third Avenue
                                                                                                                                                                                                              Tamaki, Toshimi;
Fukaya, Masahiro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (212)370-1622
                                                                                                                                                          Okumura, Hajime;
                                                                                                                                                                                             Takemura,
Biochimica et Biophysica Acta.
                                                                                                       Nishiyama, Makoto;
Horinouchi, Sueharu and
                                                                                                                                           Kawamura, Yoshiya;
                                                                                                                                                                              Tayama, Kenji;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawamura,
                                                                                                                                                                                                                                                                                  Acetobacter altoacetigenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okumura, Hajime and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukaya, Masahiro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takemura, Hiroshi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible (NEC PC-9801 ES)
                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herbert
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                                                                                                                                                                                             Hiroshi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alcohol Dehydrogenase Complex, Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structural Gene of Membrane-Bound
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                                                                                                                                                                                                                                                                                                                     purified protein having a molecular weight of about 72,000
                                                                                                                                                                                                                                                                                                                                                      N-terminal sequences of the
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US-07-985-458-3
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Best Local Similarity 20.4
Matches 78; Conservative
                                                                                                    245
                                                                                                                                      428
526 TGGDLLFQGLANGEFHAYDATNG
                                302 APEDQNEHEILN---VAVGGTNG
                                                                  483 DSPEAKQAFVKDLK-----
                                                                                                                                                                       205
                                                                                                                                                                                                       379 AKTGEFI-----SGKNYVYVNWASGLDPKTG-----RPIYNPDALYTLTGKEWYGIPGD 427
                                                                                                                                                                                                                                                                          319 SIVALKPETGEYVWHFQETPMDQWDFTSDQQIMTLDLPINGETRHVIVHARKNGFFYIID 378
                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                              259
                                                                                                                                                                                                                                         153 MPVGDWLWPAIWMLPEDWVYGGW-----PRSGEIDIIETIGNRD--FKNTGGEFLGIQ-K 204
                                                                                                                                                                                                                                                                                                                                                                                                                212 GNGGSEF-----GARGFVSAFDAETGKVDWRFFTVP-----NPKNEPDAASDSVLMN
                                                                                                                                                                                                                                                                                                                                                                              98 GVLDVWAMYGACTNTDNNGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 GGGNSEFQLYTQDGANSFVR------DGKLFIKPTLLADNINPQTGAPFGTD-FMYN
                                                                                      WSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWE---WGKPWLPQYENDNPWAGGTNL 301
                                                                                                                                     LGGHNFAAMAFSP-----KTGLVYIPAQQVPFLYTNQVGGFTPHPDSWNLGLDMNKVGIP 482
                                                                                                                                                                                                                                                                                                            ----IPPAMSARVRTFQ-----KYSFTHGR-----
                                                                                                                                                                     MG----STMHWGPGWDDNRYWLTSLP-----
                                                                                                                                                                                                                                                                                                                                            KAYQTWSPTGAWTRQGGGGTVWDSIVYDPVADLVYLGVGNGSPWNYKYRSEGKGDNLFLG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 112.5; DB 1;
Pred. No. 0.013;
7; Mismatches 113;
548
                                321
                                                                    -GWIVAWDPQKQAEAW--RVDHKGPWNGGILA 525
                                                                                                                                                                                                                                                                                                          ----- 152
                                                                                                                                                                   --KHSDDWNYGDNFHTFWFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 738;
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Search completed: September 16, 2003, 11:30:26 Job time: 42.6247 secs

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Title:
Perfect score:
Sequence:
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No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB DB
                                                                                                                                                                                                                                                                                                                                104.5
103.5
102.5
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174.5
175.5
112.5
112.5
110
100
100
106
106
106
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Match
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Gapop 10.0 , Gapext 0.5
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2240
1 MRWTLVVLCLLEGEGFAFTD......DDEGDNNAMQVDYIRVYKRN 384
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            BB
    E13B_BACCI
EXEL RHIME
EXEL RHIME
EXEL RHIME
DHET_ACEPO
XYNA_RUMEL
GUB_BACLI
NANH_VIBCH
KRE6_YEAST
GUB_PAEPO
DHET_ACEEU
OSTA_HAEIN
XYND_RUMEL
GUB_CLOTM
FDXG_HAEIN
XYNX_CLOTM
FDXG_HAEIN
XYNX_CLOTM
ANYB_PAEPO
XYNA_THESA
YY07_METJA
EXAA_PSEAE
GLGB_ECOLI
SKN1_YEAST
BRU1_SOYBN
MS1P_CRIGR
MOKB_SCHPO
TREZ_MYCTU
MANB_ASPNG
MS1P_RAT
MYCO_STRCI
AGGAA_VIBS7
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(without alignments)
666.771 Million cell updates/sec
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Compugen Ltd
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P45798 rhodothermu
033680 rhizobium m
092392 rhizobium m
P28036 acetobacter
P29126 ruminococcu
P27051 bacillus li
P37060 vibrio chol
P32486 saccharomyc
P4579 paenibacill
      P444846
P448484
P448484
P87923317
P879233
P29716
P46448
P367023
P21543
P38535
P38535
P38536
P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
7 pseudomonas
2 escherichia
6 saccharomyc
4 glycine max
8 cricetulus
4 schizosacch
9 mycobacteri
3 aspergillus
3 aspergillus
3 rattus morus
0 streptomyce
9 vibrio sp.
                                                                                                                                                                                                                       6 haemophilus
7 ruminococcu
0 bacillus am
3 candida alb
6 clostridium
8 haemophilus
4 candida alb
5 clostridium
5 paenibacili
7 thermoanaer
6 methanococc
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	P16218 clostridium	P49609 gracilaria	Q54794 spirulina p	P26501 pseudomonas					P02675 homo sapien		Q00310 candida alb	P12616 actinomyces	

ALIGNMENTS

P23903; 01-NOV-1991 (Rel. 20, Created)
1991 (Rel. 20, Last sequenc
(Rel. 38, Last annotation update)
beta-glucan endohydrolase) ((1->3)-beta-glucanase Al).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
D=1397;
[1] SEQUENCE FROM N.A., AND SEQUENCE OF 39-52.
THE SECOND OF 19 D
MEDLINE=90185240; PubMed=2311931;
Yahata N., Watanabe T., Nakamura Y., Yamamoto Y., Kamimiya S.,
Circulans WI-12 ":
Gene 86:113-117(1990).
CELLULAR WALLS
-i- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
SIMILARITY: BELONGS TO FAMILY
This SWISS-PROT entry is convright. It is produced through a collaboration
ween the Swiss Institute of Bioinformatics and the EMBL outstati
use by non-profit institutions as long as its content is in no way
ified and this statement is not removed. Usage by and for commerce
tities requires a license agreement (See http://
or send an email to licensegisb-sib.ch).
InterPro; IPRUUU757; Glyco_hydro_16. Pfam; PF00722; Glyco hydro 16; 1.
S01034; GLYC
SIGNAL 1 38
39 682
007 33. 354K5
082 AA; /3465 MW;
15.7%; Score 351 nilarity 26.2%; Pred. No.
0; Conservative 44
YFDG
424 NLIWQDEFNGTTLDTSKWNYETGYYLNNDPATWGWGNAELQHYINSTQNYYVQDGKLNIK 483

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
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Spilliaert R., Hreggyidsson G.O., Kristjansson
Eggertsson G., Palsdottir A.;
"Cloning and sequencing of a Rhodothermus maring
for a thermostable beta-glucanase and its expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4,1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GUB_RHOMR
P45798;
                   Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Bacteroidetes;
Crenotrichaceae; Rhodoth
NCBI_TaxID=29549;
                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodothermus marinus (Rhodothermus obamensis).
Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
     CHAIN
                                                                                                                     PIR;
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                                                                               Pram;
                                                             PROSITE;
                                                                                                   [nterPro;
                                                                                                                                                                                                                                                                                                                        FUNCTION: SHOWS ACTIVITY ON LICHENAN, BETA-GLUCAN AND LAMINARIN BUT NOT ON CMC CELLULOSE OR XYLAN.

CAPALITIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.

MISCELLANEOUS: The enzyme has a temperature optimum of 85 degrees Celsius and a pH optimum of 7.0.

SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biochem. 224:923-930(1994).
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                                               Pro; IPR000757; Glyco_hydro_16.
PF00722; Glyco_hydro_16; 1.
PE; PS01034; GLYCOCYT
                                                                                                                                   U04836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFDEPFYLIMNLAVGGNFDGGRTP---
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                                       Glycosidase;
                                                                                                                                     AAA60459.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                         GLYCOSYL_HYDROL_F16;
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                                     Signal
   BETA-GLUCANASE
                       POTENTIAL.
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EXSH. RHIME
ID EXSH.R
AC 033680
DT 30-MAY
DT 30-MAY
DT 30-MAY
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DE Endo-1
DE biosyn
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OOS Rhizob
OO Rhizob
OO RHIZOB
OO NCBLIT
RN [1]
RP SEQUEN
RX MEDLIN
RA YORK
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RN STRAIN
RA SOJOIN
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXSH_RHIME O33680;
                                                                                                                                                                                               STRAIN-1021
   MEDLINE=98226741;
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"The Rhizobium meliloti exoK gene and prsD/prsE/exsH components of independent degradative pathways which production of low-molecular-weight succinoglycan."; Mol. Microbiol. 25:117-134(1997).
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endo-1,3-1,4-beta-glycanase exsH (EC 3.2.1.
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-21899394; PubMed-11902715;
York G.M., Walker G.C.;
"The Rhizobium meliloti exoK gene
                                                                                                                                                                                                                                                                                                                                                                          Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; Alphaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                          biosynthesis protein exsH) EXSH OR RB1055 OR SMB20932
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                              Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
112; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSEFQLYTQDG-ANSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MRWTLVVLCLLFGEGFAFTD-----WDQYHIVWQDEFDYF---DGAKWQHEVTATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WYDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WVYGG--WPRSGEIDIIETIG-NRD-----FKNTGGEFLGIQKMGSTMHWGPGWDDNRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRRTAFLLSVLIGCSMLGSDRSDKAPHWE----LVWSDEFDYSGLPDPEKWDYDVGGHGWG
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163
286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
PubMed=9560202;
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163
33145
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PROTON DONOR (BY SIMILARITY)
; 7215C33624135191 CRC64;
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                                                                                                                                                                                                                                                                                                                                                              Sinorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Succinoglycan
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contribute to
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                                                                                   from
                                                                                                              Gouzy
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                                                                                   the
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                                                                                                              J.
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RESULT 4
EGLC_RHIME
ID EGLC_RHIME
AC Q9Z3Q2;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U89164; AAB64093.1; -.
EMBL; AL603645; CAC49455.1; -.
PIR; G95973; G95973.
InterPro; IPR000757; Glyco_hydro_16.
InterPro; IPR001343; Hemlysn_Ca_bind.
Pfam; PF00722; Glyco_hydro_16; 1.
Pfam; PF007353; hemolysinCabind; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00313; CABNDNGRPT.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; FALSE_NEG.

PROSITE; PS00330; HEMOLYSIN_CALCIUM; FALSE_NEG.

Exopolysaccharide synthesis; Glycosidase; Hydrolase; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: Exopolysaccharide biosynthesis.
SUBCELLULAR LOCATION: SECRETED. PROBABLY BY A TYPE-III S
SYSTEM.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 VWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAPFGTDFMYNGVLDVWAMYGA-CTNTDNNGCYRTGAAGDIPPAMSARVRTFQKYSFTHG
                                                                                                                                                               GL--
                                                                                                                                                                                                            GCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRVY 381
                                                                                                                                                                                                                                                                                                                                                                         IATVH--SNETGSRTSIENSVKVAD----ASGFHTYGVLWTEEEIVWYFDDAAIARADTP
                                                                                                                                                                                                                                                                                                                                                                                                                              GSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFLGIQKM 205
                                                                                                                                                                                                                                                                                                                    YPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YFEMRADMPDDQGVWPAFWLLPAD---GSWP--PELDVVEMRGQD--SNT-----V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              465 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275
349
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                            STANDARD
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349
354
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21.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 175.5;
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NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6C8482366E9E8CA8
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                            465
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                                                                                                                                                            -ADGSEMKIDYIKAY
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Query Match
Best Local S
Matches 82
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RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
sinorhizobum mediloti pSyma megaplasmid.";
"Proc. Natl. Acad. Sci. U.S.A. 98:9883-9886(2001).
C.-i-FUNCTION: CLEAVES HIGH MOLECULAR WEIGHT SUCCINOGLYCAN TO YIELD LMW
CC SUCCINOGLYCAN. DYNAMICALLY REGULATES THE MOLECULAR WEIGHT
CLISTRIBUTION OF SUCCINOGLYCAN BY CLEAVING NASCENT SUCCINOGLYCAN
ONLY DURING A LIMITED PERIOD AFTER ITS SYNTHESIS, PERHAPS BEFORE
C DISTRIBUTION STATE (BY SIMILARITY).
C -1- PATHWAY: Exopolysaccharide biosynthesis.
C -1- PATHWAY: Exopolysaccharide biosynthesis.
                                                                                       DOMAIN
ACT_SITE
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CXM1-105;
STRAIN=CXM1-105;
MEDLINE=99413305; PubMed=10485295;
Charmona L.A., Yurgel S.N., Kelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endo-1,3-1,4-beta-glycanase eglC (EC 3.2.1.-) (Succinoglycanal Control of the Synthesis protein eglC).
EGGC OR RA0864 OR SMA1587.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                     EMBL; AJ225896; CAB38101.1; -.
EMBL; ABC07/273; AAK65522.1; -.
PIR; H95369; H95369.
InterPro; IPR000757; Glyco_hydro_16.
InterPro; IPR001343; Hemlysn_Ca_bind.
Pfam; PF00722; Glyco_hydro_16; 1.
Pfam; PF007353; hemolysincabind; 3.
                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                      SEQUENCE
                                                                                                                                                              Exopolysaccharide synthesis;
Complete proteome.
                                                                                                                                                                                                    PRINTS; PR00313; CABNDNGRPT.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; FALSE_NEG.

PROSITE; PS00330; HEMOLYSIN_CALCIUM; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The eff-482 locus of Sinorhizobium meliloti CXMI-105 that influences symblotic effectiveness consists of three genes encoding an endoglycanase, a transcriptional regulator and an adenylate cyclase."; mol. Gen. Genet. 261:1032-1044(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=1021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21396509; PubMed=11481432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES
 l Similarity
82; Conserv
                                                                                                          275
349
3354
                                                                      52
465 AA;
                                                                                           465
349
354
52
                                                                      49614 MW;
               7.5%;
22.7%;
                 Score 167; DB 1
Pred. No. 2e-06;
                                                                      PROTON DONOR (BY SIMILARI
I -> T (IN REF. 1)
; 12CB879AED9E6558 CRC64;
                                                                                                                                                                                 Glycosidase;
                                                                                                                                              CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keller
                                                                                                                           NUCLEOPHILE (BY SIMILARITY)
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                                                                                                                                                                                 Hydrolase;
                                  1.
                                                                                                          SIMILARITY)
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                                  Length
                                                                                                                                                                                   Plasmid;
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Conservative

40;

Mismatches

117;

Indels 122;

Gaps

19;

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01-AUG-1992 (Rel. 23,
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                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                        DHET_ACEPO P28036;
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   Acetobacteraceae;
NCBI_TaxID=439;
                                                                                                                                                                                                                                                                                                                                                                            Bactería; Proteobactería;
                                                                                                                                                                                                                                                                                                                                                                                                            Alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                      MEDLINE=91159482; PubMed=2001402;
                                                                                                                                                                                                                                                                                                                                                                                     Acetobacter polyoxogenes.
                                                                                                                         SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PERIPI SPACE (POTENTIAL).
SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE
                                                                                                                SIMILARITY: Contains 1 cytochrome c domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDDWNYGDNFHTFWFDWSPNGLRFFYDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTNTDNNGCYRTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDELQWY------VNPT----YQPTASANPFS---VTDGVLTITAKPASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQTGA-PFGTDFMYNGVLDVWAMYGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FANTSADQLHANQFSLALDRSVLTQTFSDDFNTLQLSDGTSGVWDPKYWWAPEKGATLTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DWVYGGWPRSGEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKH
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 BAA00528.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                              Acetobacter
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Last annotation updat
[acceptor] precursor
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                                                                                                                                                                                                                                                                                                                                                                        Alphaproteobacteria;
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aldehyde +
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Matches 78
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01-DEC-1992
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28-FEB-2003
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BINDING
BINDING
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InterPro; IPR002372; Bac_PQQ_repeat.
InterPro; IPR000345; CytC_heme_bind
pfam; PF01011; Bacterial_PQQ; 3.
SMART; SM00564; PQQ; 3.
MEDLINE=92261318; pubMed=1584021; Zhang J.-X., Flint H.J.; Zhang J.-X., Flint H.J.; and bifunctional xylanase encoded by the xynA gene of the rumen cellulolytic bacterium Ruminococcus flavefaciens 17 comprises two dissimilar domains linked by an asparagine/glutamine-rich sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                       SEQUENCE FROM N.A.
STRAIN=17;
                                                                                                                                           Bifunctional
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                                                                                     NCBI_TaxID=1265;
                                                                                                            Bacteria;
                                                                                                                       Ruminococcus
                                                                                                                                                                                                 XYNA_ROMFL
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78; Conser
                                                                                                                                                                                                                                                      TGGDLLFQGLANGEFHAYDATNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAYQTWSPTGAWTRQGGGGTVWDSIVYDPVADLVYLGVGNGSPWNYKYRSEGKGDNLFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVLDVWAMYGACTNTDNNGC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNGGSEF - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGNSEFQLYTQDGANSFVR------DGKLFIKPTLLADNINPQTGAPFGTD-FMYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00190;
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                                                                                                                                                                                                                                                                                                                                                              MG----STMHWGPGWDDNRYWLTSLP-----
                                                                                                                                                                                                                                                                                                                                                                                     AKTGEFI-----SGKNYVYVNWASGLDPKTG-----RPIYNPDALYTLTGKEWYGIPGD
                                                                                                                                                                                                                                                                                                                                                                                                                               SIVALKPETGEYVWHFQETPMDQWDFTSDQQIMTLDLPINGETRHVIVHARKNGFFYIID
                                                                                                                                                                                                                                                                         APEDQNEHEILN --- VAVGGTNG
                                                                                                                                                                                                                                                                                                 DSPEAKQAFVKDLK - - -
                                                                                                                                                                                                                                                                                                                     WSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWE---WGKPWLPQYENDNPWAGGTNL
                                                                                                                                                                                                                                                                                                                                                                                                          MPVGDWLWPAIWMLPEDWVYGGW-----PRSGEIDIIETIGNRD--FKNTGGEFLGIQ-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----IPPAMSARVRTFQ-----KYSFTHGR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00364;
                                                                                                                                                                                                                                                                                                                                          LGGHNFAAMAFSP-----KTGLVYIPAQQVPFLYTNQVGGFTPHPDSWNLGLDMNKVGIP
                                                                                                          Firmicutes;
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(Rel.
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                                                                                                                                         (Rel. 24, Created)
(Rel. 24, Last sequence up
(Rel. 41, Last annotation
endo-1,4-beta-xylanase X)
                                                                                                                      flavefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQQ; Heme; Periplasmic;
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CYTOCHROME_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACTERIAL_PQQ_1;
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                                                                                                            Clostridia;
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7; Mismatches
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                                                                                                                                                                                                  PRT;
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1E2B6ED7BCD92AF6 CRC64;
                                                                                                                                                                                                                                                       548
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                                                                                                                                                                update)
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SIMILARITY).
                                                                                                            Lachnospiraceae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     -VVVHAK------
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                                                                                                                                              3.2.1.8).
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Matches 77
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InterPro; IPR00137; Glyco_hydro_11.
Pfam; PP00331; Glyco_hydro_10; 1.
Pfam; PF00457; Glyco_hydro_11; 1.
PRINTS; PR00134; GLHYDRLASE10.
PRINTS; PR00914; GLHYDRLASE11.
SMART; SM00633; Glyco_10; 1.
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PROSITE; PS00591; GLYCOSYL_HYDROL_F10; 1.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1;

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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PATHWAY: Xylan degradation.

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS
G (FAMILY 11 OF GLYCOSYL HYDROLASES).

SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS
F (FAMILY 10 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                          FWEWGKPWLPQYEN-DNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPAL
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                                                                                                                                NRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVD
                                                                                                                                                                                                                          LPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGE-----FLGIQKMGSTMHWGPGWDD
                                                                                                                                                                                                                                                                                                                    CYRTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWL------WPAIWM
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Pred. No. 0.13;
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PROTON DONOR (BY SIMILARITY).
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Glyco_hydro_16 7; GLHYDRLASE16

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RESULT 7
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Ja; 1GBG; \\
InterPro; IP:
Pfam; Pr'
PRT''
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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01-AUG-1992 (Rel. 23, Createu,
01-AUG-1992 (Rel. 23, Last sequence update,
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
                                                                                                                                                                                                                                                                                                                                                                                                       Juncosa M., Pons J., Dot T., Querol E., Planas A.; "Identification of active site carboxylic residues in Elicheniformis 1,3-1,4-beta-D-glucan 4-glucanohydrolase site-directed mutagenesis."; J. Biol. Chem. 269:14530-14535(1994).
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P27051;
01-AUG-1992
                                                                        EMBL;
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                                                                                                    entities requires a 
or send an email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucanohydrolase from mutagenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning, expression and nucleotide sequence of the endo-beta-1,3-1,4-D-glucanase gene from Bacillus licheniformis Predictive structural analyses of the encoded polypeptide."; Eur. J. Biochem. 197:337-343(1991).
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96063718; PubMed=7589539;
                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
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Planas A., Juncosa M., Lloberas J.,
"Essential catalytic role of Glul34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Querol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94237863; PubMed=8182059;
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                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
MISCELLANEOUS: BETA-GLUCANASES OF BACILIUS HAVE A SUBSTRATE RANGI SIMILAR TO LICHENASE OF GERMINATING BARLEY.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
; PF00722; GI
rs; PR00737;
                                                        X57279; CAA40547.1;
S15388; S15388.
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                                                                                                   email to license@isb-sib.ch).
                                          07-DEC-95.
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in endo-beta-1,3-1,4-D-glucan 4-
mis as determined by site-directe
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residues in Bacillus
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                      SLGEMRLSLTSPSYNKFDCGENRSVQTYGYGLYEVNMK-----
                                             LFLSLSTFAASASAQTGGSFYEPFNNYN--TGLWQKADGYSNGNMFNC
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idase; Signal; 3D-stru
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Pred. No. 0.04
12; Mismatches
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NUCLEOPHILE.
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185% OF WILD-TYPE ACTIVITY.

23 % OF WILD-TYPE ACTIVITY.

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26 % OF WILD-TYPE ACTIVITY.

27 % OF WILD-TYPE ACTIVITY.

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21 COMPLETE LOSS OF ACTIVITY.

22 % OF WILD-TYPE ACTIVITY.

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24 % OF WILD-TYPE ACTIVITY.

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28-FEB-2003 (Rel. 41,
Sialidase precursor (
NANH OR VC1784
                                                                                                                                                      Taylor G.L., Vimr "Purification, cr of neuraminidase
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Wasserman S.S., Kaper J.B.,
"Role of Vibrio cholerae notoxin.";
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Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam
Gill S.R., Nelson K.E., Read T.D., Tettellin H., Richardson
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infect. [2]
                       lectin-like domains in addition to the catalytic domain.";
Structure 2:535-544(1994).
-j- FUNCTION: CLEAVES THE TERMINAL SIALIC ACID (N-ACETYL NEURAMINIC
ACID) FROM CARBOHYDRATE CHAINS IN GLYCOPROTEINS PROVIDING FREE
                                                                                                                                                                                                                           Vimr E.R., Lawrisuk L., Galen J.E., Ke "Cloning and expression of the Vibrio nanH in Escherichia coli";
J. Bacteriol. 170:1495-1504(1988).
                                                                                                                                                                                                                                                                       SEQUENCE OF 1-44 1
STRAIN=Classical (
MEDLINE=88169467;
                                                                      "Crystal structure of Vibrio
                                                                                                                                                                                        CHARACTERIZATION,
MEDLINE=92389334;
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Fraser C.M.;
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MEDLINE=20406833; PubMed=10952301;
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MEDLINE=92112298;
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Vibrionaceae;
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                                                                                                                                  Mol. Biol.
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                                                                                                         CRYSTALLOGRAPHY (2
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eae; Vibrio.
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recursor (EC 3.2.1.18) (Neu
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                                                                                                                                                       Vimr E.R., Garman E.F., Laver W.G
n, crystallization and preliminary
dase from Vibrio cholerae and Salmo
                                                                                                                                 226:1287-1290(1992).
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Ogawa 395 / ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ogawa 395 / ATCC; PubMed=1730470;
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                                                         Laver W.G., Vimr E.R., Taylor G.L. rio cholerae neuraminidase reveals dition to the catalytic domain.";
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                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                        EMBL; M83562; AAA27546.1; --
EMBL; AE004255; AAF94933.1; ALT_INIT.
EMBL; M19268; AAA27547.1; --
PIR; A27734; A27734.
PIR; A43866; A43866.
PDB; 1KIT; 05-JUN-97.
TIGR; VC1784; --
                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                  InterPro; IPR002860; GH_BNR.
Pfam; PF02012; BNR; 4.
Hydrolase; Glycosidase; Sign
                                                                                                                                                                                                                                                                                                                                                                                                                                        GROWTH-PHASE-DEPENDENT MECHANISM.
-!- SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES
-!- SIMILARITY: CONTAINS 4 BNR repeats.
                                                                                                                                                                                                                                                                                            Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MICROBIAL INFECTIONS. NANH FACILITATES CHOLERA TOXIN BINDING TO HOST INTESTINAL EPITHELIAL CELLS BY CONVERTING CELL SURFACE POLYSIALOGANGLIOSIDES TO GMI MONGGANGLIOSIDES. CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal static residues in oliopsaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates. copactor: CALCIUM.

SUBCULTULAR LOCATION: Secreted.
INDUCTION: MAY BE CONTROLLED BY SIALIC ACID AVAILABILITY AND A GEOGRAPH - DHASE - NEPROMENTEM METGRANTEM
   Signal; Repeat;
                                                                                                                                                                                                                                 SIALIDASE.
BNR 1.
BNR 2.
BNR 3.
BNR 4.
PROTON DONOR (BY SIMILARITY).
S -> L (IN REF. 3).
                                                                                                                                                                                                                                                                                                  Calcium; 3D-structure;
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Best Local (
                       Matches
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44 VTATGGGNSE---FQLYTQDGAN---SFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYN 97
                       82;
                               Similarity
                       Conservative
                                                     4449
453
461
470
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394
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413
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337
341
349
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362
376
                                                     4.9%;
                      ; Score 109; DI
; Pred. No. 0.2;
31; Mismatches
                             DB 1;
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                       107;
                                    Length 781;
                       Indels 128;
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20;

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RESULT 9

KRE6_YEAST
ID KRE6_Y
AC P32486
DT 01-OCT
DT 01-OCT
DT 01-OCT
DT 028-FEB
DE Beta-g
DE resist
GN KRE6 0
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OC Eukary
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RP SEQUEN
RY (3)
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KRE6 OR YPR159W.
                                                                                                                                                        MEDLINE-97313271; PubMed-9169875;
Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E., Churcher C.M., Coster F., Davis R., Davis R.W., Chung E., Churcher C.M., Coster F., Davis K., Davis R.W., Dietaltrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A., Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau Hall J., Hebling U., Heumann K., Hilbert H., Hillier L., Bundar M., Floeth M., Fortin R., Helbert H., Hillier L., Bundar M., Heumann K., Hilbert H., Hillier L., Bundar M., Botth C., Bundar M., Helbert H., Hillier L., Bundar M., Botth C., Bundar M., Helbert H., Hillier L., Bundar M., Botth C., Bundar M., Helbert H., Hillier L., Bundar M., Botth C., Bundar M., Helbert H., Hillier L., Bundar M., Bundar M., Helbert H., Hillier L., Bundar M., Bundar M., Helbert H., Hillier L., Bundar M., Bundar M., Bundar M., Helbert H., Hillier L., Bundar M., Bund
 Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., Kromp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D., Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Scherens B., Schramm S., Schroeder M., Scicu A.M., Tettelin H., Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H., Hani J.;
                                                                                                                                                                                                                                                                           MEDLINE=97313271; Pub
Bussey "
                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95176711; PubMed-7871892; Roemer T.D., Fortin N., Bussey H.; "DNA sequence analysis of a 10.4 kbp chromosome XVI positions GPH1 and SGV identifies two novel tRNA genes."; Yeast 10:1527-1530(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Yeast beta-glucan synthesis: KRE6 encodes a predicted membrane protein required for glucan synthesis in vivo synthase activity in vitro.";
Proc. Natl. Acad. Sci. U.S.A. 88:11295-11299(1991).
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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NCBI_TaxID=4932;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
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Roemer T., Paravicini G., Payton M.A., Bussey H.;

"Characterization of the yeast (1->6)-beta-glucan biosynthetic components, Kre6p and Skn1p, and genetic interactions between the PKCl pathway and extracellular matrix assembly.";

J. Cell Biol. 127:567-579(1994).

-i- FUNCTION: INVOLVED IN THE SYNTHESIS OF (1->6)- AND (1->3)-BETA-D-GLUCAN POLYMERS OF THE YEAST CELL WALL IN VIVO. IT IS REQUIRED FOR FULL ACTIVITY OF BETA-GLUCAN SYNTHASE IN VITRO. IT MAY BE A BETA-GLUCAN SYNTHASE, PART OF A MULTIPROTEIN GLUCAN SYNTHASE OR
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sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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"Two beta-glycanase genes are clustered in Bacillus polymyxa:
molecular cloning, expression, and sequence analysis of genes
encoding a xylanase and an endo-beta-(1,3)-(1,4)-glucanase.";
J. Bacteriol. 173:7705-7710(1991).

-1. CATALYTIC ACTYVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages
in beta-D-glucans containing 1,3 and 1,4-bonds.

-1. MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGE
SIMILAR TO LICHENASE OF GERMINATING BARLEY.

-1. SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
                                                                                                                                                                                                                                                                                                     HSSP: P23904; 1CPN.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                                                                                                                                                                             EMBL; X57094; CAA40379.1;
PIR; S19012; S19012.
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the European Bioinformatics Institute. There a
use by non-profit institutions as long as i
modified and this statement is not removed. Us
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P45797;
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Bacteria; Firmicutes; Bacillales; Paenibacillaceae;
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                                                       PQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKYSF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PDGCINRGGDPALQKPWS------NGDW-YNDAMRKFFDARGNWKWTWDDEGDN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAMOVDYIRVYK 382
                                                                                                                                                                                                     27
129
133
56
238 ;
                                                                                                                                                                                                                                                                                            Glycosidase;
                                                                                                                                                Conservative
                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                               26
238
129
133
85
26919
                                                                                                                                                            4.7%;
22.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  660
                                                                                                                                                                                                                                                                                         Signal
                                                                                                                                                                                                        WW.
                                                                                                                                               32;
                                                                                                                                             Score 106; DB
Pred. No. 0.09
32; Mismatches
                                                                                                                                                                                                                  BETA-GLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                      COCF7B4EA5D40E8C CRC64;
                            -GEYRSTNNYG-YGLYEVSMKPAKNTGIVSSFFTYTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238
                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib
                                                                                                                                                           ; DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no rest
                                                                                                                                                                        1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                92;
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paenibacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                             96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                       .ch/announce/
                                                                                                                                             Gaps
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Query Match
Best Local S
Matches 78
                                                   CHAIN
DOMAIN
BINDING
BINDING
METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q44002; 0079:
15-DEC-1998
15-DEC-1998
28-FEB-2003
                                                                                                                                                                                                                                                            EMBL; Y09480; CAA70688.1; -. HSSP; Q924J7; 1FLG.
InterPro. Trocci
                                                                                                                                                                                                  InterPro; IPR001479; Bac_PQQ.
InterPro; IPR002372; Bac_PQQ_repeat.
InterPro; IPR000345; CytC_heme_bind.
Pfam; PP01011; Bacterial_PQQ; 3.
SMART; SM00564; PQQ; 3.
                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases -i- CATALYTIC ACTIVITY: A primary alcohol + acceptor - a
                                                                                                                                     SIGNAL
                                                                                                                                                Oxidoreductase;
                                                                                                                                                              PROSITE; PS00363; BACTERIAL_PQ0_1; 1. PROSITE; PS00364; BACTERIAL_PQ0_2; 1. PROSITE; PS00190; CYTOCHROME_C; 1.
                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                             SPACE (POTENTIAL).
-i- SIMILARITY: BELONGS TO THE BACTERIAL PQQ DEHYDROGENASE FAMILY.
-i- SIMILARITY: Contains 1 cytochrome c domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reduced acceptor.
-!- COFACTOR: PQQ AND HEME (BY SIMILARITY).
-!- SUBUNIT: HETEROTETRAMER (DEHYDROGENASE, CYTOC SMALLER UNKNOWN SUBUNITS) THAT FORMS THE ALCC COMPLEX (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thurner C.A.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-DES11 / DSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acetobacteraceae; Gluconacetobacter. NCBI_TaxID=33995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHET_ACEEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acetobacter europaeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alcohol dehydrogenase (acceptor) precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
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               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             007952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KHTATTNIP----STPGKIMMNLWNGTGVDSWLGSYNGANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYG----DNFHTFWFDWSPNGLRFFVDD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENQALLDVPYPLIDANPWWVDFWEWG----KPWLPQYENDNP
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                                                     36
635
651
654
655
739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                            35
739
739
651
655
80944
                                                                                                                                              PQQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6160;
            4.7%;
                                                                                                                                                   Heme;
                                                      WW;
                                                                                                                                                 Periplasmic;
            Score 106; DB Pred. No. 0.34;
                                                   HEME (COVALENT) (BY SIMILARITY).
HEME (COVALENT) (BY SIMILARITY).
IRON (HEME AXIAL LICAND) (BY SIM
E681BB237ACB91F4 CRC64;
                                                                                                         ALCOHOL DEHYDROGENASE [ACCEPTOR].
CYTOCHROME C-LIKE.
                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.
                                                                                                                                                Membrane;
                         DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOCHROME, AND TWO
E ALCOHOL DEHYDROGENASE
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                         Length 739;
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                                                                                                                                              signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an aldehyde
                                                                 SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration –
MBL outstation –
                                                                                                                                                                                                                                                                                                                                                                                            outstation
                                                                                                                                                                                                                                                                                                                                         .ch/announce/
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78;

Conservative

Pred. No. 0.3 37; Mismatches

118;

Indels

146;

Gaps

20;

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RESULT 12
OSTA_HAEIN
ID OSTA_HAEIN
AC P44846;
DT 01-NOV-1995
DT 01-NOV-1995
DT 01-NOV-1995
DT 028-FEB-2003
DE OFGANIC SOLO
GN IMP OR OSTA
OS HAEMOPHILUS
OC PASTEUVIELLA
OX NCBI_TAXID=
RN [1]
RP SEQUENCE FR
RC STRAIN=Rd /
RX MEDLINE=953
RA Fleischmann
RA Kerlavage A
RA KKENNey K.
RA SCOTT J.D.
RA Gnehm C.L.,
RA Fine L.D. /
RA Gnehm C.L.,
RA Fine L.D. /
RA Gnehm C.L.,
RA Fine L.D. /
RA Gnehm C.L.,
RA Gray C., Fool
RA Langen H.,
RA Gray C., Fool
RA GRA GRAY C., Fool
RA GRA
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                    MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gentman C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                  Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pasteurellaceae;
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMP OR OSTA OR HI0730. Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Rd / KW20 /
MEDLINE-95350630; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                      le-genome random
   SWISS-PROT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFAAMAFSP----KTGLVYIPAQQVPFLYTNQVGGFTPHPDSWNLGLDMNKVGIPDSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGSIVALKPETGEYVWHFQETPMDQWDFTSVQQIMTLDLPINGETRHVIVHAPKNGFFYI
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                                                                                                                                                                                                                     ВΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tolerance protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus.
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32, Last sequence up
41, Last annotation
                                                                                                                                                                                                MASS SPECTROMETRY.
PubMed=10675023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCC 51907;
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copyright.
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                                                                               biogenesis. Coulombrane components
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Best Local s
Matches 83
                                                                                                                                                                                                                                                                                 XYND_RUMFL Q53317;
                                                STRAIN-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                 Ruminococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                  336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
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HAMAP; MF_01411; -; 1.
InterPro; IPR00563; OstA.
Pfam; PF03968; OstA; 1.
Pfam; PF04453; OstA_C; 1.
Outer membrane; Signal; Com
SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as last scontent is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FDYFDGAKWQHEVTATGGGNSEFQLYTQDG--ANS---FV-RDGKLFIKPTLLADNINPQ
                                                                                                                                                                                                                                                                                                      MWHARFKIHGVPVFYTPYLQLPIGDRRRSGLLIPSAGTSSQDGLWYAQPIYWNIAPNYDL
                               ------LOKPWSNGDWYNDAMRKFFD
                                                                                                                                                                                       SLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWE-WG
                                                                                                                                                                                                                                                      ---PEDWYYGGWPRSGEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLT
                                                                                                                                                                                                                                                                                                                                            --HGRVVVHA-----
                                                                                                                                                                                                                                                                                                                                                                                                                   TGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSA-RVRTFQKYSFT-
LDFNYHKYDLANGWLNFKLHSQAVR--FD
                                                                       RSTDGYANQY---
                                                                                                           KP---WLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGF-IPDGCINRGGDPA---
                                                                                                                                                   -- KRHLFYWNHNSSFLQNW
                                                                                                                                                                                                                              TFTPKYMSRRGWQANGEFRYLTSIGE--
                                                                                                                                                                                                                                                                                                                                                                                -----GDNAWAVDASEIRQYVKEEYAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              782 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NQINML-GKDAEFNLDSHDGNLTNSEYEFVGRQGR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90084 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.7%;
21.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
POTENTIAL.
ORGANIC SOLVENT TOL
84 MW; E73C8A5786B02D1B
                                                                         -- ARIAYYQPNYNFSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                            -KMPVG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 106;
Pred. No. 0.
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                                 355
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                                                                                                                                                     RLNINYTRVSDKRYFNDFDSIYG
                                                                         -- AHQFQIFDDIVNIGPYRAVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                          -DWLW----PAIWML----
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NUMPER STANDARD; PRT; 802 AA.

Q53317;

O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Xylanase/beta-glucanase precursor [Includes: Endo-1,4-beta-xylanase
(EC 3.2.1.8) (Xylanase); Endo-beta-1,3-1,4 glucanase (EC 3.2.1.73)
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase)].
XYND.
Ruminococcus flavefaciens.
Bacteria: Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;
Ruminococcus.
NCBI_TaxID=1265;
[1]
SEQUENCE FROM N.A.
STRAIN=17;
MEDLINE=9325938; PubMed=8491715;
Flint H.J., Martin J., McPherson C.A., Daniel A.S., Zhang J.-X.;
Flint H.J., Martin J., McPherson C.A., Daniel A.S., Zhang J.-X.;
Flint H.J., Martin J., McPherson C.A., Daniel A.S., Zhang J.-X.;
Flint H.J., Martin J., McPherson C.A., Daniel A.S., Zhang J.-X.;
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Best Local S
Matches 58
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InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF02018; CBM_49; 1.
Pfam; PF004157; Glyco_hydro_11; 1.
Pfam; PF007722; Glyco_hydro_16; 1.
Pfam; PF007731; GLYCO_hydro_16; 1.
PRINTS; PR00911; GLHYDRLASE16.
PRINTS; PR009737; GLHYDRLASE16.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.
PROSITE; PS01074; GLYCOSYL_HYDROL_F11_2; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
Xylan degradation; Hydrolase; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
ACT_SITE
ACT_SITE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·!- CATALYTIC ACTIVITY: Hydrolysis of in beta-D-glucans containing 1,3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BETA-1,3-1,4 GLUCANASE ACTIVITIES.
-!- CATALYTIC ACTIVITY: Endohydrolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 175:2943-2951(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucanase domains, encoded
flavefaciens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G (FAMILY 11 OF GLYCOSYL HYDROLASES). SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: Xylan degradation.
SIMILARITY: IN THE N-TERMINAL SECTION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linkages in xylans.
                                                                                                                                                                                                                                                                                                  557
    275
                                         703
                                                                                                                                                                                                                                                       153
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P23904; 1AJK.
                                                                                                                                                                                                                                                                                                                                         95
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                          MYNGVLDVWAMYGACTNTDNN--GCYRTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAK
                                       GKHEKLYDLGFDSSEAYHTYGFDWQPNYIAWYVDGREVYRATQDIPKTPGKIMMNAWPGL
                                                                                                                                                                                                                                                   MPVGDWLWPAIWMLPEDWVYGG------WPRSGEIDIIETIGNRDFKNTGGEF----
  ----WVDFWEWGKPWLPQY
                                                                                                                       FYHYGYYECSMQAMKNDGVVSSFFTYTGPS-DDNPWDEIDIEILGKNTTQVQFNYYTNGQ
                                                                                                                                                                  -----LGIQKMGST-----MHWGPGWDDN-----
                                                                                  PKHSDDWNYG----DNFHTFWFDWSPNGLRFFVDDEN--QALLDVPYP--LIDANPW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003305; CBM_CenC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 802
                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      523
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                                                                                                                                                                                                       -WYKRNAVINDGCLQLSIDQKWTNDKNPD-----WDPRYSGGEFRTNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              89091 MW;
                                                                                                                                                                                                                                                                                                                                                                                                    4.7%;
20.8%;
                                                                                                                                                                                                                                                                                            -GTPMNTSATMISDFRTGKAGDF-----FASDGWTNGK-----
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ACTIVITIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINKER.
C (BETA
                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C (BETA-GLUCANASE).
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
XYLANASE/BETA-GLUCANASE.
A (XYLANASE).
B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-THR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycosidase;
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                                                                                                                                                                                                                                                                                                                                                                            ed. No. 0.44
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of
                                                                                                                                                                                                                                                                                                                                                                                                  .44;
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
  ·-ENDNPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
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295
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Best Local
                                                                                                                                                                                                                                                                     ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hofemeister J., Kurtz A., Borriss R., Knowles J.;
"The beta-glucanase gene from Bacillus amyLoliquefaciens shows
extensive homology with that of Bacillus subtills.";
Gene 49:177-187(1986).
-I- CATALYTIC ACTIVITY: Hydrolysis of 1,4 beta-D-glycosidic linkages
-I- MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGI
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                           Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M15674; AAA87323.1;
PIR; A29091; A29091.
HSSP; P27051; 1GBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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P07980;
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus amyloliquefaciens.
Bacteria; Firmicutes; Bacil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BE 20/78;
MEDLINE=87192007; PubMed=3106158;
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01-AUG-1988
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-JUN-1994 (Rel. 29, Last annotation update)
ta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4
-3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
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FADLGFDAANAYHTYAFDWQPNSIKWYVDGQLKHTATTQIP
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                                                                                                                             MSARVR-----TFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDI
                                                                                                                                                                              LFIKPTLLADNINPQTGAPFGTDF-MYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPA 129
                                                   LYEVRMKPAKNTGIVSSFFTYTGPTE--
                                                                           IETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDD
                                                                                                     SLGEMRLALTSPSYNKFDCGENRSV-
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Pred. No. 0.13;
1; Mismatches
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NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
A76A64268A7AAAOB CRC64;
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Matches 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation of the Candida albicans homologs of Saccharomyces cerevisiae KRE6 and SKN1: expression and physiological function.";

J. Bacteriol. 179:2363-2372(1997).

-I- FUNCTION: INVOLVED IN THE SYNTHESIS OF (1->6)- AND (1->3)-BETA-D-GLUCAN POLYMERS OF THE YEAST CELL WALL IN VIVO. IT IS REQUIRED FOR FULL ACTIVITY OF BETA-GLUCAN SYNTHASE IN VITRO. IT MAY BE A BETA-GLUCAN SYNTHASE, PART OF A MULTIPROTEIN GLUCAN SYNTHASE OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-97234650; PubMed-9079924;
Mio T., Yamada-Okabe T., Yabe T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycetales; mitosporic
                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR005629; DUF338. Pfam; PF03935; DUF338; 1.
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Yamada-Okabe H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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                                                                                                                                       SEQUENCE
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SUBCELLULAR LOCATION:
SIMILARITY: STRONG, TO
                                     347
              80
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DNINPQTGAPFGTDFMYNGVLDV-WAMYGACTNT----
                                     DGSEWVLVFSDEFD------
                                                             DWDQYHIVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLA
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Pred. No. 0.54
18; Mismatches
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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657 -LILNLGISNNWAYIDWPSISFPVTFRIDYVRVYQ 690
349 AMRKFFDARGNWKW-TWDDEGDNNAMQVDYIRVYK 382
627GDDPTLTVYSQALH
289 YENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYND 348
594 VTWYEFGDNAHNFQTYGYEYLNDPETGYLRWFV
229 SDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQ 288
534 SSGKKENCGVASOSLQLAPMDIWYIPDYNWVEIYNFSVSTMNTYTGGPFQQALSATTMLN 593
186 TIGNRDFKNTGGEFLGIQKMG
474 YSYDSCDAGITPNOSSPDGISYLPGQRLNKCTCPGELHPNRGVGRGAPEIDVIEGEVMTD 533
177 RSGEIDIIE 185
420MVQSWNQLCYTQGHLEISARLPNYGNVTGLWPGLWSMGNLGRPGYLGSTDGVWP 473
127 PPAMSARVRTFQKYSFTHGRVVVHAKMP-VGDWLWPAIWMLPEDWVYGGWP
378DIHYDATKDLEWYDPDAVTTANGTLNLRMDAYKNHNLFYRSG 419

Search completed: September 16, Job time : 30.0831 secs 2003, 11:26:31

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Matches 384; Conserv
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MEDILINE-98406152; PubMed-9733802;

Beschin A., Bilej M., Hanssens F., Raymakers J., Van Dyck E.,

Revets H., Brys L., Gomez J., De Baetselier P., Timmermans M.;

"Identification and cloning of a glucan- and Lipopolysaccharide-
binding protein from Eisenia foetida earthworm involved in the
activation of prophenoloxidase cascade.";

J. Biol. Chem. 273:24948-24954(1998).

EMBL; AF030028; AAC35887.1;

EMBL; AF030028; AGC35887.1;

InterPro; IFR000757; Glyco_hydro_16.

Pfam; PF00722; Glyco_hydro_16; 1.

SEQUENCE 384 AA; 44322 MW; C90B5C94003BAD6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        077072
077072;
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                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Annelida; Cli
Lumbricina; Lumbricidae; Eisenia.
                                                                                                                                                                                                                                                                                                                                                                                                                         Eisenia foetida (Common brandling worm) (Common dung-worm).
Eukaryota: Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
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س
                                                                              MRWTLVVLCLLFGEGFAFTDWDQYHIVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQD
                                                             MRWTLVVLCLLFGEGFAFTDWDQYHIVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQD
                                                                                                                             Conservative
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                                                                                                                                        100.0%; Score 2240; DB 5; 100.0%; Pred. No. 1.9e-167;
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Last sequence update)
Last annotation update)
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Matches 346
                                                                                                                                                                                                                                                                                                              Signal.
SIGNAL
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"Distinct carbohydrate recognition domains of an earthworm molecule recognize Gram negative and Gram positive bacteria Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF395805; AAL09587.1; -.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
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01-JUN-2002 (TremBLrel. 21, Last annotation update)
Coelomic cytolytic facerory.
Lumbricus terrestris (Common earthworm).
Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
Lumbricina; Lumbricidae; Lumbricus.
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01-DEC-2001
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346; Conserv
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                                                                                                                                                                                  GANSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRT
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LAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW
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                                                                                                                             GAAGDIPPVMSARVRTFQKFSFTHGRVVVHAKMPVGDWLWPAIWMLPENWVYGGWPRSGE
                                                                                                                                                                     SRNSFVRDGKLFIKPSLLADNNNPQTGQPYGTDFMNNGVLDVWANYGACTNTDNNGCYRT
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90.1%;
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Pred. No. 1.9e
15; Mismatches
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01-OCT-2002
01-MAR-2003
QBN0N3;
01-OCT-2002
01-OCT-2002
01-MAR-2003
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"The Lipopolysaccharide and beta-1,3-Glucan Binding Prote
Opregulated in White Spot Virus-Infected Shrimp (Penaeus
stylirostris).";
J. Virol. 76:7140-7149(2002).
EMBL; AF473579; AAM73871.1; -.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; pF00722; Glyco_hydro_16; 1.
SEQUENCE 376 AA; 42610 MW; D7ADC5A310208885 CRC64;
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NCBI_TaxID=29019;
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Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Lipopolysaccharide and beta-1,3-glucan binding prot
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MEDLINE-22068042; PubMed=12072514;
                                           Q8N0N3
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(TrEMBLrel.
(TrEMBLrel.
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                                          PRELIMINARY;
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43.0%;
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22,
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Created)
Last sequence
Last annotation
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Pred. No. 1.2e:
58; Mismatches
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D7ADC5A310208885
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Q9U0G4;
Q9U0G4;
01-MAY-2000
01-MAY-2000
01-OCT-2001
                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Crustacea; Malace
Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
Astacoidea; Astacidae; Pacifastacus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2001) to the EMBL/Geni
EMBL; AF368168; AAM21213.1; -
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
SEQUENCE 366 AA; 41497 MW; 6F540.
        purification,
J. Biol. Chem.
Lee S., Wang R., Soderhall K.;

"A lipopolysaccharide and beta-1,3-glucan-binding protein fr. hemocytes of the freshwater crayfish Pacifastacus leniusculu: purification, characterization, and cDNA cloning.";

J. Biol. Chem. 275:1337-1343(2000).
                                                                                                         TISSUE-Hemocyte;
MEDLINE-20092910; PubMed-10625682;
                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                              Pacifastacus leniusculus
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"The beta-1,3-glucan
Penaeus monodon.";
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Penaeus monodon (Penoeid shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Pe
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Best Local :
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                                                                              Bachman E.S., McClay D.R.;

Molecular cloning of the first metazoan beta-1,3
of the sea urchin Strongylocentrotus purpuratus.";

Proc. Natl. Acad. Sci. U.S.A. 93:6808-6813(1996).

BMBL; U49711; AAC47235.1;
                                                                                                                                                                                   Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; E
Echinoidea; Euechinoidea; Echinacea; Echinoida; St
                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
Beta 1,3-glucanase.
                                                                       SEQUENCE
                                                                                                                                 MEDLINE=96270625; PubMed=8692900;
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                Strongylocentrotus. NCBI_TaxID=7668;
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Pro: IPR000757; Glyco_
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Similarity 42.7%;
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Dimopoulos G., Richman A., Mueller H.M., Kafatos F.C.
"Molecular immune responses of the mosquito Anopheles
bacteria and malaria parasites.";
Proc. Natl. Acad. Sci. U.S.A. 94:11508-11513(1997).
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Neoptera; Endopterygota;
NCBI_TaxID=7165;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation updat
Putative GRAM negative BACTERIA binding protein p
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles
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  THGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFLGI
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                                                                                                                                               LIFEDNFDFFDFEKWEHVNTLAGGGNWEFQWYTNNRSNSFVEDGALNIRPTLTADQ----
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                                                                                                                                                                                                                                             Conservative
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                                                 FGLDFMTSGTLSLQGSYPTDHCTNDAFYGCVRVGNRQHIVNPVKSARIRTISSFNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                  Score 703;
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9462AB490AD43A63 CRC64;
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Best Local Sin
Matches 148;
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09C236;
01-JUN-2001 (TrEMBLrel. 17, Cr
01-JUN-2001 (TrEMBLrel. 18, L
01-OCT-2001 (TrEMBLrel. 18, L
palated to beta-1, 3-glucan b
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InterPro; 1:
Fam; PF00722; G:
462 F
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Schulte U., Aign V., Ho
Schulte G., Mewes H.W
Nyakatura G., Mewes H.W
Submitted (FEB-2001) to
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Eukaryota; Fungi; Ascomycota; Pezizomy
Sordariales; Sordariaceae; Neurospora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tted (FEB-2001) to the EMBL/Gen
AL5:13445; CAC28774.1; -.
AL5:13445; CAC28774.1; -.
Pro; IPR000757; Glyco_hydro_16.
PF00722; Glyco_hydro_16; 1.
NCE 462 AA; 51868 MW; 28808
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                                                                     \textbf{AKRLRRSDESESFHTFGLEWDAKYMYFYMDNRLTQIMHVGFKAKD------DLWKMGE-F}
                                                                                                     PKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPW
                                                                                                                                                                     MPQDSTYGVWPRSGEIDIMESRGNGHDYAPGGRNL---
                                                                                                                                                                                                                                                                 GTTNASCVAHSDPKTGAM - - IPPVRSARLITKDTKTLRYGRVEVVAKLPKGDWLWPAIWM
                                                                                                                                                                                                                                                                                          NTDNNGCY----RTGAAGDIPPAMSARVRTFQXYSETHGRVVVHAKMPVGDWLWPAIWM
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36.2%;
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Last sequence update)
Last annotation updat
binding protein.
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Pred.
-TNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQK
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Best Local
OBCWI7; PRELIMINARY; PRT; 533 AA. QBCWI7; PRTLIEMBLEEL 23, Created)
01-MAR-2003 (TrEMBLEEL 23, Last sequence update)
01-MAR-2003 (TrEMBLEEL 23, Last annotation update)
PREMB-2003 (TrEMBLEEL 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribeiro J.M.C.;

"Toward the sialome of the adult female mosquito Aedes aegypti.";

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; Ar466594; AAL76017-1;

EMBL; Ar260757; Glyco_hydro_16.

InterPro: IPR000757; Glyco_hydro_16.

Pfam; PF00722; Glyco_hydro_16; 1.

SEQUENCE 371 AA; 41943 MW; IFE2E5DC7B665CE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative secreted protein.

Aedes aegypti (Yellowfever mosquito).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8T9V2;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Black eye; TISSUE-Salivary gland; Valenzuela J.G., Pham V.M., Garfield M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7159;
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                                                                                                                                                                                                                                                                                                                                                                                                                      GTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDY 377
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EKIGIQKVSSCLHFG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSFAFKYGKVEINAKLPQGDWLWPALWLLPKGDTYGYWPKSGEVDLMESRGNRNLVQ-NN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---YGEAFLKSGVINLNEGPQSQRCTDAPGWAEQIHGCYRRGSPDRILNPVRSARLRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFRTV-TPYE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSDNGLRFFVDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAPFGTDFMYNGVLDV--WAMYGACTNTDN----NGCYRTGAAGDI-PPAMSARVRTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIFQDNFNRLDRNVWQHENSLGGGGNNEFQWYSGSGRNSYIKNNHLYIRPTLTSDE----
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ilarity 35.4%;
Conservative 7
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                                                                                                                                                                                                                                                                                                                                                   381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -DNPNVRSSQCGSVSGNLFGAMFNRYQLTWTKNVIQFGINDR
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 596.5; DB 5;
Pred. No. 9.4e-39;
1; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---FSFNPWPKGSKMAPFDKEFYIVMNVAVG
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                                                                                                                                                                                                                                                                                                                                                                                             -GDAAALEVDW
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RESULT 11
Q96TU2
ID Q96TU
AC Q96TU
DT Q1-DE
DT Q1-DE
DT Q1-DE
DT Q1-DE
DT Q1-DE
COC EUKAI
OC EUKAI
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RN SEQUE
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Best Local (
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                          NON_TER
NON_TER
SEQUENCE
                                                                           Eshel D., Prusky D., Dinoor A.;
"Mixed'linked glucanase precursor of Alternaria alternata.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF282319; AAK69516.1;
InterPro; IPR000757; Glyco_hydro_16.
                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alterna NCBI_TaxID=5599;
                                                                                                                                                                                                                             Q96TU5;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                      Mixed-linked glucanase (Fragment).
Alternaria alternata.
                                                                 PROSITE;
                                                                                                                                                                                                                                                                                    Q96TU5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AE016812; AA008191.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 533 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM STRAIN-CMCP6;
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Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio vulnificus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                 PS01034;
                                                                                                                                                                                                                                                                                                                                                                     KPWSNGDWYNDAMRKFFDARGNWKWTWDDEGD-NNAMQVDYIRVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL--GIQKMGSTMHWGPGWDDNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIWMLPTDNKYGTWAASGEIDIMEAVNLKAQSDAPGAQAGDGENRIYGSLHYGKAWPDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIVGCSQTGDSASATDLYQTKKPYMLQDQPTPPSDQWQLVWVDEEDGDKINKRNWSLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y--WLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CWGGGNNEQQCYTKRARNAFVQDGYLHIVAHKESYSGPDNPEGKVGA--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGGNSEFQLYTQDGANSFVRDGKLFI----KPTLLA-DNINPQTGAPFGTDEMYNGVLD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSGQGASLP---NNINPADDFHTYAIEWEEGEIRWYVDNIHYAT-----
                           278
278 1
                                                                                                                                                                                                                                                                                                                                                                                                    QTQDEWYSQYKVDGALVNAKGAAPFDERLHLLLNLAVGGS
                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                              57; Glyco_hydro_16.
GLYCOSYL_HYDROL_F16;
                           31073 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58976 MW;
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 18.5%;
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                                                                                                                                                                                                                                                                                                                                                 ANANQKGI--DKSDFPKTMLVDYVKVYR
                                                                                                                                                                                                                             Last sequence up
                                                                                                                                                                                                                                                           Created)
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 Score 413.5;
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                                                                                                                                                                                                                                                                                   PRT;
                         B53AB7749826B22D
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                          CRC64;
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Length
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                                                                                                                                                                               Alternaria
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278;
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482

309

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RESULT 12
QOPALS
ID QOPALS
AC OPALS
AC OPALS
DT 01-OC
DT 01-JU
DE Beta-
OC Bomby
OC ELWARI
OC HOMBY
OC
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Ol-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Ol-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Beta-1,3-glucan recognition protein precursor.
Bombyx mori (Silk moth),
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycidae; Bombyx.
NCBL_TaxID=7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-Kinshu x Showa; TISSUE-Hemocyte;
MEDLINE-20138243; PubMed-10671539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
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Pfam; PF00722; Glyco_hydro_16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 silkworm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ochiai M., Ashida M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pattern-recognition protein for beta-1,3-Glucan.
the cDNA cloning of beta-1,3-glucan recognition
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                                            LGIQKMGSTMHWGP----GWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDD
                                                                                                                                                                                                                 PQTGAPFGTDEMYNGVLDVWAMYGACTNTDNNG-CYRTGAAGD--IPPAMSARVRTFQKY
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                                                                                             AFKYGRVEIRAKMPKGDWLYPEILLEPRDNIYGVRNYASGILKIASVKGNAEF-----
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SKKLYAGPIMTGSDPYRSFYLKENIGYESWN--NDFHNYTLEWRPDGITLLVDG
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55802 MW;
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6; Mismatches 99;
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BETA-1,3-GLUCAN RECOGNITION PROTEIN.

09249039F7456BF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.8e
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 390.5;
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ches 122;
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SIGNAL
CHAIN
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pfam; PF00722; Glyco_hydro_16;
SMART; SM00635; BID_2; 1.
SMART; SM00409; IG; 1.
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EMBL; S67033; AAC50453.1; -.
InterPro; IPR00343; Big_2.
InterPro; IPR000757; Glyco_hydro_16.
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto M., Aono R., Horikoshi K.;
"Structure of the 87-kDa beta-1,3-glucanase general in the service of the enzyme accumulates and properties of the enzyme accumulates are service accidentation of the gene.";
Escherichia coli carrying the gene.";
Biosci. Biotechnol. Biochem. 57:1518-1525(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; NCBI_TaxID=1397;
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Bacteria; Firmicut
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877 I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95451 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   493
                                                                                               -AVHFGGQWPTNRY-LSGEYHFPEGQTFANDYHVYSVVWEEDNIKWYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01, Created)
01, Last sequence update)
23, Last annotation updat
precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 369.5; DB 2;
Pred. No. 1.6e-20;
1; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANSYKVEA----APQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C4D2CFF93019446C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ISNKPWKNS--ATKAMLKFWDARSQWFPTWDED--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillaceae;
       GKFFFKVTRDQWYSAAAPNNP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            accumulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                877
                                                                                                                                                                                                                                                                                          -AQYS-
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in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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the periplasm of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141;
       -- NAPFDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                               SGKI
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306

617 254 569

645

194 509

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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Hichards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxter B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kelman T.J., Wei M.-H., Ibeywam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Ki Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Ki Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentalov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentalov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentalov G., Standers R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shen B.C., Siden-Kamos I., Simpson M., Skupski M.P., Smith T.,
RA Shen B.C., Siden-Kamos I., Simpson M., Skupski M.P., Smith T.,
RA Shen B.C., Siden-Kamos I., Simpson M., Skupski M.P., Smith T.,
RA Shen B.C., Shen M., Shong W., Zhou S., Zhu X., Smith H.O.,
RA Shen S., Per Ra R., Shen 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
Q9VVR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
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       Query Match
                                                                                                                           "The genome sequence of Drosophila Science 287:2185-2195(200).
EMBL; AE003519; AAF49244.1;
ElyBase; FBgn0040323; GNBP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hacapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNBP1 OR CG6895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9VVR5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9VVR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14
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                                                      IPR000757; Glyco_hydro_16.
)722; Glyco_hydro_16; 1.
492 AA; 55314 MW; C5D0E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TMQVDYVRVYK 683
          15.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382
       Score 357;
                                         1.
C5D0E5E61FABB779 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492
       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
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     5.
     Length 492;
RESULTI
Q59328
ID Q59
AC Q50
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139
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Best Local Similarity 27.3
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q59328 PRELIMINARY;
Q59328; Q9AL34;
01-NOV-1996 (TIEMBLIEL 01, C:
01-JUN-2002 (TIEMBLIEL 21, L4
01-MAR-2003 (TIEMBLIEL 23, L4
Endo-1,3(4)-beta-glucanase (E
                                                                           Zverlov V.V., Schwarz W.H.;
Submitted (FEB-2002) to the E
EMBL; X89732; CAA61884.2; -.
EMBL; A3307315; CAC27412.2; -.
HSSP; P14090; 1ULO.
InterPro; IPR003305; CBM_CenC
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-DSM 1237;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-DSM 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Schwarz W.H., Schimming Submitted (DEC-1995) to
                                         InterPro;
                                                                                                                                                                                               STRAIN-F7
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium thermocellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-DSM 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 DLS-----IANSRLD---LSERCTGTHNRIKECILHSTGSGPSGIMPPIVTPRISTKE
                                       ; IPR003305;
; IPR000757;
; IPR001119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAMQVDYIRVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KYSFTHGRVVVHAKMPVGDWLWPAIWMLP-EDWVYGGWPRSGEIDIIETIGNRDFKNTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFSVDGQVYGEMLNGFTELDENP--------RWKQGGPMAPFDKMFYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLVD----GRSLYGGP-----VLSTDAHQREDLWLSKRKISHFGDDFHTYSLDWSSNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDW------NYGDNFHTFWFDWSPNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFAFQYGRIEIRAKLPKGDWIVPLLLLEPLTEWYGQSGYESGQLRVALARGNSVLRMPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLFEETFDQLNESLWIHDVRLPLDSKDAEFVLY--DG-KAKVHDGNLVIEP-LLWSSYRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -ALKIDYVRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLGVSVGGFGDF----VDHLRTATYEKPWAN--YHPQAKLQFHQAQDQWLPTWKQP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTGAPFGTDFMYNGVLDVWAMYGACTNTDN--NGCY----RTGAAGDIPPAMSARVRTFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVWQDEFDYFDGAKWQHEV-TATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINP
                                                                                                                                                                                                                                                     (APR-2002)
                                                                                                                                                                                                                                                                                                                                                  (JUL-1995)
CBM_4_9; 4.
Glyco_hydro_16;
                                       ; CBM_CenC.
; Glyco_hydro_16.
; SLH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                    the 1
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the
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                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
(EC 3.2.1.6).
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                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                             Fuchs K.P., Staudenbauer W.L.;
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.6e-20;
ches 133;
                                                                                                                                                          databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70;
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Search completed: September 16, 2003, 11:28:43 Job time: 121.005 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.8%; Score 353; DB 2; Length 1321; Best Local Similarity 27.2%; Pred. No. 5.2e-19; Matches 100; Conservative 51; Mismatches 93; Indels 124; Gaps 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00395; SLH; 3.
Glycosidase; Hydrolase.
SEQUENCE 1321 AA; 147772 MW; A45213FF99748F0C CRC64;
                                                           377 YIRVYKRN 384
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664 YVRVYQKD 671
                                                                                                                                                                                                                                                                                                                 140 YSFTHGRVVVHAKMPVGDWLWPAIWMLPEDW-VYGGWPRSGEIDIIETIGNRDFKNTGGE 198
|: :|: :|||| :||||||:||| || ||:||:|:
502 KSWKYGKPEIRAKWPQGQGIWPAIWMMPEDEPFYGTWPKCGEIDIMELLGHEP------ 554
                                                                                                                                                                                   478 ---KEDITEPSGETYHYT-----SKLITKGK 501
                                                                                                                                                                                                                                                                                                                                                                                                                                           643 G------PQQMVVD 663
                                                                                                                                                       317 GGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVD 376
                                                                                                                                                                                                                                                                                                                                                                                                             80 DNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQK 139
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